GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 29, 2004, 08:30:39 ; Search time 2081.94 Seconds
(without alignments)
8508.338 Million cell updates/sec

Title: US-09-982-405-1
Perfect score: 433
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		432	99.8	446	6	AX055450	AX055450 Sequence
2		432	99.8	446	6	AX055704	AX055704 Sequence
3		432	99.8	446	6	AX376378	AX376378 Sequence
4		432	99.8	464	9	AF072844	AF072844 Homo sapi
5		419	96.8	467	9	AF122904	AF122904 Homo sapi
6		419	96.8	488	9	BC035931	BC035931 Homo sapi
7		419	96.8	504	9	AF172929	AF172929 Homo sapi
8		419	96.8	506	6	AR177375	AR177375 Sequence
9		419	96.8	506	6	BD131449	BD131449 cDNA enco
10		419	96.8	524	9	HSM800238	AL050163 Homo sapi
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12		419	96.8	753	6	AR220847	AR220847 Sequence
13		416.8	96.3	451	6	AR217546	AR217546 Sequence
14		416.8	96.3	451	6	BD080218	BD080218 Mammalian
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17		213	49.2	231	6	BD077448	BD077448 5'EST of
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21		147.2	34.0	16918	9	CH19F19399	AD000833 Homo sapi
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	c 36	88.4	20.4	256254	2	AC096476	AC096476 Rattus no
37		47.2	10.9	7218	6	I66494	I66494 Sequence 14
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	c 41	40.8	9.4	128906	8	AP003810	AP003810 Oryza sat
	c 42	40.8	9.4	151317	8	AP004262	AP004262 Oryza sat
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44		40.6	9.4	198468	9	AC098477	AC098477 Homo sapi
45		40.2	9.3	276710	2	AC129823	AC129823 Rattus no

ALIGNMENTS

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LOCUS AX055450 446 bp DNA linear PAT 13-JAN-2001
DEFINITION Sequence 80 from Patent WO0073452.
ACCESSION AX055450
VERSION AX055450.1 GI:12228718
KEYWORDS .
SOURCE Homo sapiens (human).
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Ashkenazi,A.J., Baker,K.P., Chan,B., Goddard,A., Godowski,P.J.,
Gurney,A.L., Hebert,C., Henzel,W., Kabakoff,R.C., Shelton,D.L.,
Tumas,D., Watanabe,C.K. and Wood,W.I.

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  TITLE     Compositions and methods for the treatment of immune related
            diseases
  JOURNAL   Patent: WO 0073452-A 80 07-DEC-2000;
            Genentech, Inc. (US)
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BASE COUNT       78 a    153 c    110 g    105 t
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  Matches  432;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        422 TAAAACAATTGA 433
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LOCUS       AX055704                 446 bp    DNA     linear   PAT 13-JAN-2001
DEFINITION  Sequence 19 from Patent WO0073348.
ACCESSION   AX055704
VERSION     AX055704.1  GI:12228835
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Baker,K.P., Goddard,A., Gurney,A.L., Hebert,C., Henzel,W.,
            Kabakoff,R.C., Shelton,D.L., Smith,V., Watanabe,C.K. and Wood,W.I.
  TITLE     Methods and compositions for inhibiting neoplastic cell growth
  JOURNAL   Patent: WO 0073348-A 19 07-DEC-2000;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
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BASE COUNT       78 a    153 c    110 g    105 t
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  Matches  432;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        182 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 241
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DEFINITION  Sequence 445 from Patent WO0168848.
ACCESSION   AX376378
VERSION     AX376378.1  GI:19170580
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Baker,K.P., Chen,J., Desnoyers,L., Goddard,A., Godowski,P.J.,
            Gurney,A.L., Pan,J., Smith,V., Watanabe,C.K., Wood,W.I. and
            Zhang,Z.
  TITLE     Secreted and transmembrane polypeptides and nucleic acids encoding
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  JOURNAL   Patent: WO 0168848-A 445 20-SEP-2001;
            Genentech, Inc. (US)
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  Best Local Similarity   100.0%;  Pred. No. 2.1e-95;
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Qy        422 TAAAACAATTGA 433
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LOCUS       AF072844                 464 bp    mRNA    linear   PRI 04-AUG-1999
DEFINITION  Homo sapiens membrane protein DAP10 (DAP10) mRNA, complete cds.
ACCESSION   AF072844
VERSION     AF072844.1  GI:5690193
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 464)
  AUTHORS   Wu,J., Song,Y., Bakker,A.B., Bauer,S., Spies,T., Lanier,L.L. and
            Phillips,J.H.
  TITLE     An activating immunoreceptor complex formed by NKG2D and DAP10
  JOURNAL   Science 285 (5428), 730-732 (1999)
  MEDLINE   99357865
   PUBMED   10426994
REFERENCE   2  (bases 1 to 464)
  AUTHORS   Wu,J., Lanier,L.L. and Phillips,J.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-JUN-1998) Immunobiology, DNAX Research Institute, 901
            California Avenue, Palo Alto, CA 94304, USA
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Best Local Similarity 100.0%;  Pred. No. 2e-95;
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Qy          2 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 61
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Qy        422 TAAAACAATTGA 433
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LOCUS       AF122904                 467 bp    mRNA    linear   PRI 10-AUG-1999
DEFINITION  Homo sapiens membrane protein DAP10 (DAP10) mRNA, splice variant,
            complete cds.
ACCESSION   AF122904
VERSION     AF122904.1  GI:5714435
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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  AUTHORS   Wu,J., Song,Y., Bakker,A.B., Bauer,S., Spies,T., Lanier,L.L. and
            Phillips,J.H.
  TITLE     An activating immunoreceptor complex formed by NKG2D and DAP10
  JOURNAL   Science 285 (5428), 730-732 (1999)
  MEDLINE   99357865
   PUBMED   10426994
REFERENCE   2  (bases 1 to 467)
  AUTHORS   Wu,J., Lanier,L.L. and Phillips,J.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-JAN-1999) Immunobiology, DNAX Research Institute, 901
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  Best Local Similarity   99.3%;  Pred. No. 3.1e-92;
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Qy        182 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 241
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Db        189 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 248

Qy        242 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCC---AAGATGGCAAA 298
              |||||||||||||||||||||||||||||||||||||||||||||   ||||||||||||
Db        249 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGAAGATGGCAAA 308

Qy        299 GTCTACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTG 358
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Db        309 GTCTACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTG 368

Qy        359 ACCCTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTG 418
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 ACCCTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTG 428

Qy        419 TAATAAAACAATTGA 433
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Db        429 TAATAAAACAATTGA 443


RESULT 6
BC035931
LOCUS       BC035931               488 bp    mRNA    linear   PRI 23-SEP-2002
DEFINITION  Homo sapiens, clone IMAGE:4701500, mRNA.
ACCESSION   BC035931
VERSION     BC035931.1  GI:23271012
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 488)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONTECH
            cDNA Library Preparation: CLONTECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA  94305
            Web site:       http://www-shgc.stanford.edu
            Contact:  (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
            R. M.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAL Plate: 37 Row: a Column: 10
            This clone was selected for full length sequencing because it
            passed the following selection criteria: GenomeScan gene
            prediction.
FEATURES             Location/Qualifiers
     source          1..488
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4701500"
                     /tissue_type="Lung"
                     /clone_lib="NIH_MGC_77"
                     /lab_host="DH10B"
                     /note="Vector: pDNR-LIB"
BASE COUNT       111 a    157 c    112 g    108 t
ORIGIN

  Query Match             96.8%;  Score 419;  DB 9;  Length 488;
  Best Local Similarity   99.3%;  Pred. No. 3.1e-92;
  Matches  432;  Conservative    0;  Mismatches    0;  Indels    3;  Gaps    1;

Qy          2 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 61
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Db         18 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 77

Qy         62 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 137

Qy        122 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 181
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Db        138 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 197

Qy        182 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 257

Qy        242 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCC---AAGATGGCAAA 298
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Db        258 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGAAGATGGCAAA 317

Qy        299 GTCTACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTG 358
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Db        318 GTCTACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTG 377

Qy        359 ACCCTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTG 418
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 ACCCTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTG 437

Qy        419 TAATAAAACAATTGA 433
              |||||||||||||||
Db        438 TAATAAAACAATTGA 452


RESULT 7
AF172929
LOCUS       AF172929               504 bp    mRNA    linear   PRI 27-OCT-1999
DEFINITION  Homo sapiens transmembrane adapter protein KAP10 (KAP10) mRNA,
            complete cds.
ACCESSION   AF172929
VERSION     AF172929.1  GI:5738198
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 504)
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  AUTHORS   Chang,C., Dietrich,J., Harpur,A.G., Lindquist,J.A., Haude,A.,
            Loke,Y.W., King,A., Colonna,M., Trowsdale,J. and Wilson,M.J.
  TITLE     Cutting edge: KAP10, a novel transmembrane adapter protein
            genetically linked to DAP12 but with unique signaling properties
  JOURNAL   J. Immunol. 163 (9), 4651-4654 (1999)
  MEDLINE   99458917
   PUBMED   10528161
REFERENCE   2  (bases 1 to 504)
  AUTHORS   Wilson,M.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-JUL-1999) Pathology, University of Cambridge, Tennis
            Court Rd., Cambridge CB2 1QP, United Kingdom
FEATURES             Location/Qualifiers
     source          1. .504
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /chromosome="19"
                     /map="19q13.1"
     gene            1. .504
                     /gene="KAP10"
     CDS             92. .373
                     /gene="KAP10"
                     /codon_start=1
                     /product="transmembrane adapter protein KAP10"
                     /protein_id="AAD50293.1"
                     /db_xref="GI:5738199"
                     /translation="MIHLGHILFLLLLPVAAAQTTPGERSSLPAFYPGTSGSCSGCGS
                     LSLPLLAGLVAADAVASLLIVGAVFLCARPRRSPAQEDGKVYINMPGRG"
BASE COUNT      106 a    166 c    119 g    113 t
ORIGIN

  Query Match             96.8%;  Score 419;  DB 9;  Length 504;
  Best Local Similarity   99.3%;  Pred. No. 3.1e-92;
  Matches  432;  Conservative    0;  Mismatches    0;  Indels    3;  Gaps    1;

Qy          2 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         44 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 103

Qy         62 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        104 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 163

Qy        122 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 181
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Db        164 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 223

Qy        182 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        224 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 283

Qy        242 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCC---AAGATGGCAAA 298
              ||||||||||||||||||||||||||||||||||||||||||||   ||||||||||||
Db        284 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGAAGATGGCAAA 343

Qy        299 GTCTACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTG 358
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Db        344 GTCTACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTG 403

Qy        359 ACCCTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTG 418
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        404 ACCCTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTG 463

Qy        419 TAATAAAACAATTGA 433
              |||||||||||||||
Db        464 TAATAAAACAATTGA 478


RESULT 8
AR177375
LOCUS       AR177375                506 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 69 from patent US 6312922.
ACCESSION   AR177375
VERSION     AR177375.1  GI:17919730
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 506)
  AUTHORS   Edwards,J.-B.Dumas.Milne., Duclert,A. and Bougueleret,L.
  TITLE     Complementary DNAs
  JOURNAL   Patent: US 6312922-A 69 06-NOV-2001;
FEATURES             Location/Qualifiers
     source          1. .506
                     /organism="unknown"
BASE COUNT      101 a    171 c    115 g    119 t
ORIGIN

  Query Match             96.8%;  Score 419;  DB 6;  Length 506;
  Best Local Similarity   99.3%;  Pred. No. 3.1e-92;
  Matches  432;  Conservative    0;  Mismatches    0;  Indels    3;  Gaps    1;

Qy          2 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         50 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 109

Qy         62 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        110 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 169

Qy        122 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        170 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 229

Qy        182 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        230 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 289

Qy        242 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAG---ATGGCAAA 298
              ||||||||||||||||||||||||||||||||||||||||||||||||   ||||||||
Db        290 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGAATATGGCAAA 349

Qy        299 GTCTACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTG 358
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        350 GTCTACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTG 409

Qy        359 ACCCTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTG 418
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        410 ACCCTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTG 469

Qy        419 TAATAAAACAATTGA 433
              |||||||||||||||
Db        470 TAATAAAACAATTGA 484


RESULT 9
BD131449
LOCUS       BD131449                506 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  cDNA encoding secretory protein.
ACCESSION   BD131449
VERSION     BD131449.1  GI:23226394
KEYWORDS    JP 2002502605-A/63.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 506)
  AUTHORS   Bougueleret,L., Duclert,A. and Edwards,J.B.D.M.
  TITLE     cDNA encoding secretory protein
  JOURNAL   Patent: JP 2002502605-A 63 29-JAN-2002;
            GENSET
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002502605-A/63
            PD   29-JAN-2002
            PF   09-FEB-1999 JP 2000530603
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            10-AUG-1998 US    60/096116,04-SEP-1998 US    60/099273 PI   LYDIE
            BOUGUELERET,AYMERIC DUCLERT,JEAN BAPTISTE DUMAS MILNE  PI   EDWARDS
            PC   C12N15/09,C12N15/09,C07K14/47,C07K16/18,C12M1/00,C12N1/15, PC
             C12N1/19,
            PC   C12N1/21,C12N5/10,C12P21/02,C12Q1/68//G06F17/30,C12N15/00, PC
             C12N5/00,
            PC   C12N15/00
            CC   Von Heijne matrix
            CC   score 12.3
            CC   seq HILFLLLLPVAAA/QT
            FH   Key             Location/Qualifiers
            FT   CDS             98. .376
            FT   sig_peptide     98. .151
            FT   polyA_signal    471. .476
            FT   polyA_site      491. .506.
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT      101 a    171 c    115 g    119 t
ORIGIN

  Query Match             96.8%;  Score 419;  DB 6;  Length 506;
  Best Local Similarity   99.3%;  Pred. No. 3.1e-92;
  Matches  432;  Conservative    0;  Mismatches    0;  Indels    3;  Gaps    1;

Qy          2 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         50 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 109

Qy         62 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        110 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 169

Qy        122 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        170 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 229

Qy        182 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        230 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 289

Qy        242 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAG---ATGGCAAA 298
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Db        290 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGAATATGGCAAA 349

Qy        299 GTCTACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTG 358
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Db        350 GTCTACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTG 409

Qy        359 ACCCTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTG 418
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        410 ACCCTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTG 469

Qy        419 TAATAAAACAATTGA 433
              |||||||||||||||
Db        470 TAATAAAACAATTGA 484


RESULT 10
HSM800238
LOCUS       HSM800238               524 bp    mRNA    linear   PRI 18-FEB-2000
DEFINITION  Homo sapiens mRNA; cDNA DKFZp586C1522 (from clone DKFZp586C1522);
            partial cds.
ACCESSION   AL050163
VERSION     AL050163.1  GI:4884161
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 524)
  AUTHORS   Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-MAR-1999) MIPS, Am Klopferspitz 18a, D-82152
            Martinsried, GERMANY
COMMENT     Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
            sequenced by BMFZ (Biomedical Research Center at the Charite,
            Berlin/Germany) within the cDNA sequencing consortium of the German
            Genome Project.
            This clone (DKFZp586C1522) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
            information about the clone and the sequencing project is available
            at http://www.mips.biochem.mpg.de/proj/cDNA/.
FEATURES             Location/Qualifiers
     source          1. .524
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="RZPD:DKFZp586C1522"
                     /db_xref="taxon:9606"
                     /chromosome="19"
                     /clone="DKFZp586C1522"
                     /tissue_type="uterus"
                     /clone_lib="586 (synonym: hute1). Vector pSport1; host
                     DH10B; sites NotI + SalI/MluI"
                     /dev_stage="adult"
     gene            1. .524
                     /gene="DKFZp586C1522"
     CDS             <1. .396
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                     /note="unknown"
                     /codon_start=1
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                     /protein_id="CAB43303.1"
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                     /translation="LDTSRVTSAIATSLLPHSSSGLLWTTVLCQTPARPQSTMIHLGH
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                     VGAVFLCARPRRSPAQEDGKVYINMPGRG"
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     polyA_site      504
                     /gene="DKFZp586C1522"
BASE COUNT      106 a    176 c    121 g    121 t
ORIGIN

  Query Match             96.8%;  Score 419;  DB 9;  Length 524;
  Best Local Similarity   99.3%;  Pred. No. 3.1e-92;
  Matches  432;  Conservative    0;  Mismatches    0;  Indels    3;  Gaps    1;

Qy          2 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 126

Qy         62 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 186

Qy        122 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 181
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Db        187 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 246

Qy        182 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 241
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Db        247 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 306

Qy        242 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCC---AAGATGGCAAA 298
              ||||||||||||||||||||||||||||||||||||||||||||||   ||||||||||||
Db        307 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGAAGATGGCAAA 366

Qy        299 GTCTACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTG 358
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Db        367 GTCTACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTG 426

Qy        359 ACCCTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTG 418
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 ACCCTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTG 486

Qy        419 TAATAAAACAATTGA 433
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Db        487 TAATAAAACAATTGA 501
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RESULT 11
BC046348

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LOCUS       BC046348               551 bp    mRNA    linear   PRI 10-FEB-2003
DEFINITION  Homo sapiens, clone IMAGE:5229680, mRNA.
ACCESSION   BC046348
VERSION     BC046348.1  GI:28277217
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 551)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JAN-2003) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site: http://www.nisc.nih.gov/
            Contact: nisc_mgc@nhgri.nih.gov
            Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
            Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
            Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
            Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
            Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
            McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
            Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
            Young,A., Zhang,L.-H. and Green,E.D.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 93 Row: l Column: 23
            This clone was selected for full length sequencing because it
            passed the following selection criteria: Hexamer frequency ORF
            analysis, GenomeScan gene prediction.
FEATURES                Location/Qualifiers
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                        /mol_type="mRNA"
                        /db_xref="taxon:9606"
                        /clone="IMAGE:5229680"
                        /tissue_type="Pancreas, Spleen, adult pooled"
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  Best Local Similarity   99.3%;  Pred. No. 3.1e-92;
  Matches  432;  Conservative    0;  Mismatches    0;  Indels    3;  Gaps    1;

Qy          2 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 61
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Db        199 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 258

Qy         62 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 121
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Db        259 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 318

Qy        122 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 181
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Db        319 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 378

Qy        182 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 438

Qy        242 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCC---AAGATGGCAAA 298
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGAAGATGGCAAA 366

Qy        299 GTCTACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTG 358
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Db        367 GTCTACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTG 426

Qy        359 ACCCTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTG 418
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 ACCCTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTG 486

Qy        419 TAATAAAACAATTGA 433
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Db        487 TAATAAAACAATTGA 501
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RESULT 12
AR220847

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LOCUS       AR220847               753 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 88 from patent US 6426186.
ACCESSION   AR220847
VERSION     AR220847.1  GI:23327724
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 753)
  AUTHORS   Jones,K.A., Volkmuth,W. and Walker,M.G.
  TITLE     Bone remodeling genes
  JOURNAL   Patent: US 6426186-A 88 30-JUL-2002;
FEATURES                Location/Qualifiers
     source             1. .753
                        /organism="unknown"
BASE COUNT      157 a    260 c    178 g    157 t      1 others
ORIGIN
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  Best Local Similarity   99.3%;  Pred. No. 3.1e-92;
  Matches  432;  Conservative    0;  Mismatches    0;  Indels    3;  Gaps    1;

Qy          2 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 258

Qy         62 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 121
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Qy        122 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 181
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Qy        182 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 241
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Db        379 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 438

Qy        242 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCC---AAGATGGCAAA 298
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Db        439 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGAAGATGGCAAA 498

Qy        299 GTCTACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTG 358
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Qy        359 ACCCTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTG 418
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Qy        419 TAATAAAACAATTGA 433
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Db        619 TAATAAAACAATTGA 633


RESULT 13
AR217546
LOCUS       AR217546                 451 bp    mRNA    linear   PAT 25-SEP-2002
DEFINITION  Sequence 7 from patent US 6416973.
ACCESSION   AR217546
VERSION     AR217546.1  GI:23317338
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 451)
  AUTHORS   Bakker,A.B.H., Phillips,J.H. and Lanier,L.L.
  TITLE     Nucleic acids encoding mammalian cell membrane protein MDL-1
  JOURNAL   Patent: US 6416973-A 7 09-JUL-2002;
FEATURES             Location/Qualifiers
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ORIGIN

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  Best Local Similarity 99.3%;  Pred. No. 1.1e-91;
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Qy          2 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 61
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Db         15 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 74

Qy         62 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 121
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Db         75 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 134

Qy        122 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 181
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Db        135 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 194

Qy        182 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 241
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Db        195 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 254

Qy        242 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGGCAAAGTC 301
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Qy        362 CTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTGTAA 421
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Qy        422 TAAAACAATTGA 433
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RESULT 14
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LOCUS       BD080218                 451 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Mammalian cell membrane proteins; related reagents.
ACCESSION   BD080218
VERSION     BD080218.1  GI:22625821
KEYWORDS    JP 2001512017-A/4.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 451)
  AUTHORS   Bakker,A.B.H., Jr,J.H.P. and Lanier,L.L.
  TITLE     Mammalian cell membrane proteins
  JOURNAL   Patent: JP 2001512017-A 4 21-AUG-2001;
            SCHERING CORP
COMMENT     OS   Unknown
            PN   JP 2001512017-A/4
            PD   21-AUG-2001
            PF   31-JUL-1998 JP 2000505298
            PR   01-AUG-1997 US    08/904905,29-OCT-1997 US    60/063717 PR
            15-DEC-1997 US    08/990820,16-DEC-1997 US    60/069692 PR
            12-JUN-1998 US    60/089168
            PI   ALEXANDER B H BAKKER,JOSEPH H PHILIPPS JR,LEWIS L LANIER PC
            C12N15/09,A61K38/00,A61K39/395,A61K39/395,A61K48/00,A61P37/02, PC
            A61P43/00,
            PC   C07K14/705,C07K16/28,C07K19/00,C12N1/15,C12N1/19,C12N1/21, PC
             C12N5/10,
            PC   C12Q1/68,G01N33/15,G01N33/50,G01N33/566,C12N15/00,A61K37/02,
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BASE COUNT       79 a    154 c    111 g    107 t
ORIGIN

  Query Match           96.3%;  Score 416.8;  DB 6;  Length 451;
  Best Local Similarity 99.3%;  Pred. No. 1.1e-91;
  Matches  429;  Conservative    0;  Mismatches    2;  Indels    1;  Gaps    1;

Qy          2 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 61
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Db         15 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 74

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Qy        182 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 241
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Db        195 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 254

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Db        255 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGGCAAAGTC 314

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Qy        362 CTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTGTAA 421
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Db        375 CTCTCATCCTGGATGGTGTGTGGT-GCACAGGAAACCCCGCCCCAACTTTTGGATTGTAA 433
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Qy        422 TAAAACAATTGA 433
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Db        434 TAAAACATTTGA 445
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RESULT 15
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DEFINITION  Homo sapiens membrane protein DAP10 mRNA, complete cds.
ACCESSION   AF285447
VERSION     AF285447.1  GI:11093806
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 345)
  AUTHORS   Wu,J., Song,Y., Bakker,A.B., Bauer,S., Spies,T., Lanier,L.L. and
            Phillips,J.H.
  TITLE     An activating immunoreceptor complex formed by NKG2D and DAP10
  JOURNAL   Science 285 (5428), 730-732 (1999)
  MEDLINE   99357865
   PUBMED   10426994
REFERENCE   2  (bases 1 to 345)
  AUTHORS   Yim,D., Jie,H.B., Sotiriadis,J., Kim,Y.S., Kim,K.S.,
            Rothschild,M.F., Lanier,L.L. and Kim,Y.B.
  TITLE     Molecular cloning and characterization of pig immunoreceptor DAP10
            and NKG2D
  JOURNAL   Immunogenetics 53 (3), 243-249 (2001)
  MEDLINE   21291702
   PUBMED   11398969
REFERENCE   3  (bases 1 to 345)
  AUTHORS   Yim,D., Jie,H.-B., Sotiriadis,J., Kim,Y.-S. and Kim,Y.B.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JUL-2000) Microbiology & Immunology, Finch University
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            North Chicago, IL 60064, USA
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                     /cell_type="PBMC"
     CDS             32. .313
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                     /protein_id="AAG29425.1"
                     /db_xref="GI:11093807"
                     /translation="MIHLGHILFLLLLPVAAAQTTPGERSSLPAFYPGTSGSCSGCGS
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ORIGIN
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Query Match 75.2%; Score 325.8; DB 9; Length 345;
Best Local Similarity 98.6%; Pred. No. 2.3e-69;
Matches 340; Conservative 0; Mismatches 2; Indels 3; Gaps 1;

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Qy         79 GCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAGAGATCATCACTCCCTGC 138
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Db         61 GCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACCCCAGGAGAGAGATCATCACTCCCTGC 120

Qy        139 CTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCCCTCTCTCTGCCGCTCCT 198
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Qy        199 GGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATCGTGGGGGCGGTGTTCCT 258
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Db        181 GGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATCGTGGGGGCGGTGTTCCT 240

Qy        259 GTGCGCACGCCCACGCCGCAGCCCCGCCC---AAGATGGCAAAGTCTACATCAACATGCC 315
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Db        241 GTGCGCACGCCCACGCCGCAGCCCCGCCCAAGAAGATGGCAAAGTCTACATCAACATGCC 300

Qy        316 AGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGAC 360
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Job time : 2089.94 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 29, 2004, 08:55:20 ; Search time 1706.35 Seconds
(without alignments)
6167.457 Million cell updates/sec

Title: US-09-982-405-1
Perfect score: 433
Sequence: 1 gctctggaccacagtcctct.....gattgtaataaaacaattga 433

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
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9: gb_est1:*
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11: gb_htc:*
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13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	6	409	94.5	661	12	BI521021	BI521021 603081602
	7	406.4	93.9	795	10	BG545810	BG545810 602573087
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c	13	385	88.9	410	9	AA829607	AA829607 oe50b04.s
c	14	384	88.7	407	9	AA699808	AA699808 zj94c05.s
c	15	382	88.2	407	9	AA894359	AA894359 oj16h09.s
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c	19	360	83.1	371	9	AI308984	AI308984 qo81g09.x
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	27	233	53.8	1052	12	BM925115	BM925115 AGENCOURT
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	33	191	44.1	395	12	BM734647	BM734647 MONO1_11_
	34	188.4	43.5	260	12	BI836780	BI836780 603084847
c	35	159.2	36.8	250	10	BE856224	BE856224 7f90f02.x
c	36	126	29.1	163	10	BG370452	BG370452 nai33g09.
	37	126	29.1	193	10	BG151113	BG151113 nai33g09.
c	38	118.8	27.4	460	10	BF419129	BF419129 UI-R-BJ2-
	39	111.6	25.8	414	9	AA204202	AA204202 mu28a10.r
	40	111.6	25.8	415	4	BX511604	Bx511604 RZPD Mus
	41	111.6	25.8	440	11	AK008005	AK008005 Mus muscu
	42	111.6	25.8	913	12	BG869011	BG869011 602784637
	43	110.6	25.5	390	9	AA822679	AA822679 vw14f07.r
	44	109.4	25.3	403	14	W13188	W13188 mb31f12.r1
	45	104	24.0	261	9	AV061864	AV061864 AV061864

ALIGNMENTS

RESULT 1
BI599958
LOCUS BI599958 488 bp mRNA linear EST 07-SEP-2001
DEFINITION 603251025F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5302567 5', mRNA sequence.
ACCESSION BI599958
VERSION BI599958.1 GI:15492897
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 488)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11766 row: b column: 08

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          High quality sequence stop: 488.
FEATURES             Location/Qualifiers
     source          1. .488
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5302567"
                     /tissue_type="hypothalamus"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_96"
                     /note="Organ: brain; Vector: pBluescriptR (modified
                     pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
                     ); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTVN-3',
                     size-selected for  average insert size 2.3 kb and
                     normalized to ROT 5. This is a primary library enriched
                     for full-length  clones and constructed using the
                     Cap-trapper method (Carninci, in preparation).  Library
                     constructed by M. Brownstein (NIMH/NHGRI, National
                     Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT       96 a    163 c    117 g    112 t
ORIGIN

  Query Match             99.4%;  Score 430.4;  DB 12;  Length 488;
  Best Local Similarity   99.8%;  Pred. No. 9.3e-96;
  Matches  431;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 61
              ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db         23 CTCTGGACCACAGTCCTCTGCCAGTCCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 82

Qy         62 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 142

Qy        122 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 202

Qy        182 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 262

Qy        242 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGGCAAAGTC 301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGGCAAAGTC 322

Qy        302 TACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGACC 361
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        323 TACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGACC 382

Qy        362 CTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTGTAA 421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 CTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTGTAA 442

Qy        422 TAAAACAATTGA 433
              ||||||||||||
Db        443 TAAAACAATTGA 454


RESULT 2
AI148117/c
LOCUS       AI148117                 424 bp    mRNA    linear   EST 26-OCT-1998
DEFINITION  qb43e08.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:1702886 3',
            mRNA sequence.
ACCESSION   AI148117
VERSION     AI148117.1  GI:3675799
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 424)
  AUTHORS   NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute / National Institute of Neurological
            Disorders and Stroke, Brain Tumor Genome Anatomy Project
            (CGAP/BTGAP), Tumor Gene Index
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
            Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 533    Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham.
FEATURES             Location/Qualifiers
     source          1. .424
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1702886"
                     /tissue_type="glioblastoma (pooled)"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Brn23"
                     /note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCATATCTTTTTTTTTTTTTTTTTTTTTTT
                     T 3']; double-stranded cDNA was ligated to Eco RI
                     adaptors (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of  the modified pT7T3 vector.
                     Library is normalized, and was constructed  by Bento
                     Soares and M.Fatima Bonaldo."
BASE COUNT       99 a    105 c    147 g     73 t
ORIGIN

  Query Match             96.5%;  Score 418;  DB 9;  Length 424;
  Best Local Similarity   100.0%;  Pred. No. 1e-92;
  Matches  418;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         16 CCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTGGGTCACATCCTCTT 75
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 CCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTGGGTCACATCCTCTT 365

Qy         76 CCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAGAGATCATCACTCCC 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 CCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAGAGATCATCACTCCC 305

Qy        136 TGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCCCTCTCTCTGCCGCT 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 TGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCCCTCTCTCTGCCGCT 245

Qy        196 CCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATCGTGGGGGCGGTGTT 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 CCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATCGTGGGGGCGGTGTT 185

Qy        256 CCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGGCAAAGTCTACATCAACATGCC 315
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 CCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGGCAAAGTCTACATCAACATGCC 125

Qy        316 AGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGACCCTCTCATCCTGGAT 375
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 AGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGACCCTCTCATCCTGGAT 65

Qy        376 GGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTGTAATAAAACAATTGA 433
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 GGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTGTAATAAAACAATTGA 7


RESULT 3
BI832920
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LOCUS       BI832920                884 bp    mRNA    linear   EST 04-OCT-2001
DEFINITION  603090735F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5229680 5',
            mRNA sequence.
ACCESSION   BI832920
VERSION     BI832920.1  GI:15944470
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 884)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11578  row: e  column: 09
            High quality sequence stop: 509.
FEATURES             Location/Qualifiers
     source          1. .884
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5229680"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_120"
                     /note="Organ: pooled pancreas and spleen; Vector:
                     pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
                     source anonymous pool of spleen and pancreas from 28 yo
                     male.  Library is oligo-dT primed and directionally cloned
                     (EcoRV  site is destroyed upon cloning).  Average insert
                     size 1.5 kb, insert size range 1-2.5 kb.  Library is
                     normalized and enriched for  full-length clones and was
                     constructed by C. Gruber (Invitrogen). Research Genetics
                     tracking code 025. Note: this is a NIH_MGC Library."
BASE COUNT      224 a    322 c    190 g    148 t
ORIGIN

  Query Match             96.0%;  Score 415.8;  DB 12;  Length 884;
  Best Local Similarity   98.9%;  Pred. No. 4.4e-92;
  Matches  430;  Conservative    0;  Mismatches    2;  Indels    3;  Gaps    1;

Qy          2 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 125

Qy         62 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 185

Qy        122 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 245

Qy        182 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 305

Qy        242 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCC---AAGATGGCAAA 298
              |||||||||||||||||||||||||||||||||||||||||||||   ||||||||||||
Db        306 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGAAGATGGCAAA 365

Qy        299 GTCTACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTG 358
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 GTCTACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTG 425

Qy        359 ACCCTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTG 418
              ||||||||||||||||||||||||||||||||||||||||||||||| |||||||| ||||||
Db        426 ACCCTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGACCCAACTTTCGGATTG 485

Qy        419 TAATAAAACAATTGA 433
              |||||||||||||||
Db        486 TAATAAAACAATTGA 500


RESULT 4
AA829510/c
LOCUS       AA829510                459 bp    mRNA    linear   EST 31-MAR-1998
DEFINITION  od27f06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1369187 3',
            mRNA sequence.
ACCESSION   AA829510
VERSION     AA829510.1  GI:2902609
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 459)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
            Ph.D., Gerald Marti, M.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 511    Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham.
FEATURES             Location/Qualifiers
     source          1. .459
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1369187"
                     /tissue_type="germinal center B cell"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_GCB1"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-),
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                     (NCI) and Dr. Gerald Marti (CBER).  cDNA synthesis was
                     primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCCTCATTTTTTTTTTTTTTTT-3'
                     ]. Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT      101 a    117 c    153 g     88 t
ORIGIN

  Query Match             95.9%;  Score 415.2;  DB 9;  Length 459;
  Best Local Similarity   98.6%;  Pred. No. 5.1e-92;
  Matches  430;  Conservative    0;  Mismatches    3;  Indels    3;  Gaps    1;

Qy          1 GCTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        452 GCTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCT 393

Qy         61 GGGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGA 120
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 GGGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGA 333

Qy        121 GAGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTC 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 GAGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTC 273

Qy        181 CCTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCAT 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 CCTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCAT 213

Qy        241 CGTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCC---AAGATGGCAA 297
                ||||||||||||||||||||||||||||||||||||||||||||||   ||||||||||
Db        212 CGTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGAAGATGGCAA 153

Qy        298 AGTCTACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCT 357
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 AGTCTACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCT 93

Qy        358 GACCCTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATT 417
                ||||||| |||||||||||||||||||||||||||||||| ||||||||| ||||||||||
Db         92 GACCCTCGCATCCTGGATGGTGTGTGGTGGCACAGGAAGCCCCGCCCCGACTTTTGGATT 33

Qy        418 GTAATAAAACAATTGA 433
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Db         32 GTAATAAAACAATTGA 17
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RESULT 5
BI753833
LOCUS       BI753833                517 bp    mRNA    linear   EST 25-SEP-2001
DEFINITION  603027514F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5197971 5',
            mRNA sequence.
ACCESSION   BI753833
VERSION     BI753833.1  GI:15745411
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 517)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11495  row: l  column: 04
            High quality sequence stop: 478.
FEATURES             Location/Qualifiers
     source          1. .517
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5197971"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_114"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: EcoRV (destroyed); RNA source anonymous pool of 6
                     male brains, age range 23-27 yo. Library is oligo-dT
                     primed and directionally cloned (EcoRV site is destroyed
                     upon cloning). Average insert size 1.5 kb, insert size
                     range 1-3 kb. Library is normalized and enriched for
                     full-length clones and was constructed by C. Gruber
                     (Invitrogen). Research Genetics tracking code 019. Note:
                     this is a NIH_MGC Library."
BASE COUNT      139 a    152 c    120 g    106 t
```

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ORIGIN

  Query Match          95.9%;  Score 415.2;  DB 12;  Length 517;
  Best Local Similarity   98.8%;  Pred. No. 5.3e-92;
  Matches  429;  Conservative    0;  Mismatches    3;  Indels    2;  Gaps    1;

Qy          2 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 61
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          9 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 68

Qy         62 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 121
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 128

Qy        122 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 181
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 188

Qy        182 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 241
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 248

Qy        242 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCC--CAAGATGGCAAAG 299
              |||||||||||||||||||||||||||||||||||||||||||||  ||  ||||||||||||
Db        249 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCGCCCAAGAAGATGGCAAAG 308

Qy        300 TCTACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGA 359
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 TCTACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGA 368

Qy        360 CCCTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTGT 419
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 CCCTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTGT 428

Qy        420 AATAAAACAATTGA 433
              ||||||||||||||
Db        429 AATAAAACAATTGA 442
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RESULT 6
BI521021
LOCUS       BI521021                661 bp    mRNA    linear   EST 29-AUG-2001
DEFINITION  603081602F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5220793 5',
            mRNA sequence.
ACCESSION   BI521021
VERSION     BI521021.1  GI:15345813
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 661)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11555  row: c  column: 02
            High quality sequence stop: 438.
FEATURES             Location/Qualifiers
     source          1. .661
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5220793"
                     /lab_host="DH10B"
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/clone_lib="NIH_MGC_120"
/note="Organ: pooled pancreas and spleen; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of spleen and pancreas from 28 yo male. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-2.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 025. Note: this is a NIH_MGC Library."
BASE COUNT 133 a 219 c 163 g 146 t
ORIGIN

Query Match 94.5%; Score 409; DB 12; Length 661;
Best Local Similarity 99.3%; Pred. No. 1.9e-90;
Matches 422; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

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Qy         12 CAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTGGGTCACATCC 71
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTGGGTCACATCC 60

Qy         72 TCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAGAGATCATCAC 131
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAGAGATCATCAC 120

Qy        132 TCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCCCTCTCTCTGC 191
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCCCTCTCTCTGC 180

Qy        192 CGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATCGTGGGGGCGG 251
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATCGTGGGGGCGG 240

Qy        252 TGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCC---AAGATGGCAAAGTCTACATCA 308
              |||||||||||||||||||||||||||||||||||   |||||||||||||||||||||
Db        241 TGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGAAGATGGCAAAGTCTACATCA 300

Qy        309 ACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGACCCTCTCAT 368
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGACCCTCTCAT 360

Qy        369 CCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTGTAATAAAACA 428
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTGTAATAAAACA 420

Qy        429 ATTGA 433
              |||||
Db        421 ATTGA 425
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RESULT 7
BG545810
LOCUS BG545810 795 bp mRNA linear EST 04-APR-2001
DEFINITION 602573087F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4701500 5', mRNA sequence.
ACCESSION BG545810
VERSION BG545810.1 GI:13544475
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 795)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1536 row: m column: 21
High quality sequence stop: 466.
FEATURES Location/Qualifiers
source 1. .795
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4701500"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_77"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.9 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."
BASE COUNT 200 a 230 c 224 g 141 t
ORIGIN

Query Match 93.9%; Score 406.4; DB 10; Length 795;
Best Local Similarity 99.1%; Pred. No. 8.9e-90;
Matches 430; Conservative 0; Mismatches 1; Indels 3; Gaps 2;

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Qy          2 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         19 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 78

Qy         62 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         79 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 138

Qy        122 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 198

Qy        182 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 258

Qy        242 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCC--CAAGATGGCAAAG 299
              |||||||||||||||||||||||||||||||||||||||||||||  |||||||||||||
Db        259 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCAAGAAGATGGCAAAG 318

Qy        300 TCTACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGA 359
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 TCTACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGA 378

Qy        360 CCCTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTGT 419
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        379 CCCTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCG-CCCAACTTTTGGATTGT 437

Qy        420 AATAAAACAATTGA 433
              ||||||||||||||
Db        438 AATAAAACAATTGA 451
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RESULT 8
AA516481
LOCUS AA516481 450 bp mRNA linear EST 05-JAN-1998
DEFINITION nh52a05.r1 NCI_CGAP_Pr5 Homo sapiens cDNA clone IMAGE:955952, mRNA sequence.
ACCESSION AA516481
VERSION AA516481.1 GI:2256005
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 450)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: David G. Bostwick, M.D., Rodrigo F. Chuaqui,
            M.D., Michael R. Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: David B. Krizman, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Putative full length read
            The vector to vector length is
            Insert Length: 607   Std Error: 0.00
            Seq primer: -28m13 rev1 ET from Amersham
            High quality sequence stop: 342.
FEATURES              Location/Qualifiers
     source           1. .450
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:955952"
                      /sex="male"
                      /tissue_type="prostate"
                      /lab_host="DH10B"
                      /clone_lib="NCI_CGAP_Pr5"
                      /note="Vector: pAMP10; mRNA made from normal prostatic
                      epithelial cells, cDNA made by oligo-dT priming.
                      Non-directionally cloned.  Size-selected on agarose gel,
                      average insert size 600 bp. "
BASE COUNT       79 a    153 c    111 g    107 t
ORIGIN

  Query Match             93.5%;  Score 404.8;  DB 9;  Length 450;
  Best Local Similarity   99.1%;  Pred. No. 1.9e-89;
  Matches  428;  Conservative    0;  Mismatches    2;  Indels    2;  Gaps    2;

Qy          2 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         15 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 74

Qy         62 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         75 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 134

Qy        122 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        135 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 194

Qy        182 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        195 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 254

Qy        242 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGGCAAAGTC 301
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        255 GTGGGGGCGGTGTTCCTGTGCGCACG-CCACGCCGCAGCCCCGCCCAAGATGGCAAAGTC 313

Qy        302 TACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGACC 361
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        314 TACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGACC 373

Qy        362 CTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTGTAA 421
              |||||||||||||||||||||||| ||||||||| ||||||||||||||||||||||||
Db        374 CTCTCATCCTGGATGGTGTGTGGT-GCACAGGAAACCCCGCCCCAACTTTTGGATTGTAA 432

Qy        422 TAAAACAATTGA 433
              |||||||| ||||
Db        433 TAAAACATTTGA 444


RESULT 9
AI582746/c
LOCUS       AI582746                 430 bp    mRNA    linear   EST 13-DEC-1999
DEFINITION  tn17b03.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2167853 3',
            mRNA sequence.
ACCESSION   AI582746
VERSION     AI582746.1  GI:4568643
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 430)
  AUTHORS   NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute / National Institute of Neurological
            Disorders and Stroke, Brain Tumor Genome Anatomy Project
            (CGAP/BTGAP), Tumor Gene Index
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
            Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 476   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 414
            POLYA=No.
FEATURES              Location/Qualifiers
     source           1. .430
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:2167853"
                      /tissue_type="anaplastic oligodendroglioma"
                      /lab_host="DH10B"
                      /clone_lib="NCI_CGAP_Brn25"
                      /note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a
                      modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                      strand cDNA was primed with a Not I - oligo(dT) primer [5'
                      TGTTACCAATCTGAAGTGGGAGCGGCCGCATAGGTTTTTTTTTTTTTTTTTTT
                      T 3']; double-stranded cDNA was ligated to Eco RI
                      adaptors (Pharmacia), digested with Not I and cloned into
                      the Not I and Eco RI sites of the modified pT7T3 vector.
                      Library is normalized, and was constructed by Bento
                      Soares and M.Fatima Bonaldo."
BASE COUNT      100 a    108 c    145 g     76 t      1 others
ORIGIN

  Query Match             91.8%;  Score 397.4;  DB 9;  Length 430;
  Best Local Similarity   97.6%;  Pred. No. 1.2e-87;
  Matches  414;  Conservative    0;  Mismatches    7;  Indels    3;  Gaps    1;

Qy         13 AGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTGGGTCACATCCT 72
              |||||||||||||||||| |||||||||  |||||||||||||||||||||||||||||
Db        430 AGTCCTCTGCCAGACCCTGGCCAGACCCAGTCCCACCATGATCCATCTGGGTCACATCCT 371

Qy         73 CTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAGAGATCATCACT 132
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        370 CTTCCTGCTTTTGCTCNCAGTGGCTGCAGCTCAGACGACTCCAGGAGAGAGATCATCACT 311

Qy        133 CCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCCCTCTCTCTGCC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 CCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCCCTCTCTCTGCC 251
```

```
Qy        193 GCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATCGTGGGGGCGGT 252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 GCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATCGTGGGGGCGGT 191

Qy        253 GTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCC---AAGATGGCAAAGTCTACATCAA 309
              |||||||||||||||||||||||||||||||||||   |||||||||||||||||||||
Db        190 GTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGAAGATGGCAAAGTCTACATCAA 131

Qy        310 CATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGACCCTCTCATC 369
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 CATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGACCCTCTCATC 71

Qy        370 CTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTGTAATAAAACAA 429
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         70 CTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTGTAATAAAACAA 11

Qy        430 TTGA 433
              ||||
Db         10 TTGA 7
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```
RESULT 10
BI835298
LOCUS       BI835298                754 bp    mRNA    linear   EST 04-OCT-2001
DEFINITION  603089448F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5228410 5',
            mRNA sequence.
ACCESSION   BI835298
VERSION     BI835298.1  GI:15946848
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 754)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11574  row: p  column: 11
            High quality sequence stop: 486.
FEATURES             Location/Qualifiers
     source          1. .754
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5228410"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_120"
                     /note="Organ: pooled pancreas and spleen; Vector:
                     pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
                     source anonymous pool of spleen and pancreas from 28 yo
                     male.  Library is oligo-dT primed and directionally cloned
                     (EcoRV  site is destroyed upon cloning).  Average insert
                     size 1.5 kb, insert size range 1-2.5 kb.  Library is
                     normalized and enriched for  full-length clones and was
                     constructed by C. Gruber (Invitrogen). Research Genetics
                     tracking code 025. Note: this is a NIH_MGC Library."
BASE COUNT      253 a    209 c    190 g    102 t
ORIGIN

  Query Match             91.8%;  Score 397.4;  DB 12;  Length 754;
  Best Local Similarity   99.5%;  Pred. No. 1.4e-87;
  Matches  409;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy         24 AGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTGGGTCACATCCTCTTCCTGCTTT 83
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```
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTGGGTCACATCCTCTTCCTGCTTT 60

Qy         84 TGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAGAGATCATCACTCCCTGCCTTTT 143
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAGAGATCATCACTCCCTGCCTTTT 120

Qy        144 ACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCCCTCTCTCTGCCGCTCCTGGCAG 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCCCTCTCTCTGCCGCTCCTGGCAG 180

Qy        204 GCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATCGTGGGGGCGGTGTTCCTGTGCG 263
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATCGTGGGGGCGGTGTTCCTGTGCG 240

Qy        264 CACGCCCACGCCGCAGCCCCGCCCAAGATGGCAAAGTCTACATCAACATGCCAGGCAGGG 323
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CACGCCCACGCCGCAGCCCCGCCCAAGATGGCAAAGTCTACATCAACATGCCAGGCAGGG 300

Qy        324 GCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGACCCTCTCATCCTGGATGGTGTGTG 383
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGACCCTCTCATCCTGGATGGTGTGTG 360

Qy        384 GTGGCACA-GGAACCCCCGCCCCAACTTTTGGATTGTAATAAAACAATTGA 433
              |||||||| |||||||||||||||||| ||||||||||||||||||||||
Db        361 GTGGCACAGGGAACCCCCGCCCCAACTTGTGGATTGTAATAAAACAATTGA 411
```

```
RESULT 11
AV759411
LOCUS       AV759411                687 bp    mRNA    linear   EST 19-OCT-2000
DEFINITION  AV759411 MDS Homo sapiens cDNA clone MDSEIF02 5', mRNA sequence.
ACCESSION   AV759411
VERSION     AV759411.1  GI:10917259
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 687)
  AUTHORS   Gu,J., Zhao,M., Huang,Q., Xu,X., Li,Y., Peng,Y., Song,H., Xiao,H.,
            Gu,Y., Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng
            ,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G.,
            Yang,Y., Gao,G., Zhang,Q., Chen,S., Han,Z. and Chen,Z.
  TITLE     Homo sapiens cDNA MDS clones
  JOURNAL   Unpublished
COMMENT     Contact: Zeguang Han
            Chinese National Human Genome Center at Shanghai
            351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
            201203, P. R. China
            Tel: 86-21-50801919(ex.45)
            Fax: 86-21-50801922
            Email: hanzg@chgc.sh.cn
            This clone is available at CHGC in Shanghai.
FEATURES             Location/Qualifiers
     source          1. .687
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="MDSEIF02"
                     /tissue_type="Bone marrow"
                     /cell_type="CD34+ hematopoietic stem/progenitor cell"
                     /lab_host="BM25.8"
                     /clone_lib="MDS"
                     /note="Vector: pTriplEx2; Site_1: sfiIA; Site_2: sfiIB"
BASE COUNT      132 a    228 c    150 g    177 t
ORIGIN

  Query Match             90.7%;  Score 392.8;  DB 9;  Length 687;
  Best Local Similarity   98.8%;  Pred. No. 1.9e-86;
  Matches  407;  Conservative    0;  Mismatches    2;  Indels    3;  Gaps    1;

Qy         22 CCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTGGGTCACATCCTCTTCCTGCT 81
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Db          1 CCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTGGGTCACATCCTCTTCCTGCT 60

Qy         82 TTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAGAGATCATCACTCCCTGCCTT 141
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAGAGATCATCACTCCCTGCCTT 120

Qy        142 TTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCCCTCTCTCTGCCGCTCCTGGC 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCCCTCTCTCTGCCGCTCCTGGC 180

Qy        202 AGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATCGTGGGGGCGGTGTTCCTGTG 261
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATCGTGGGGGCGGTGTTCCTGTG 240

Qy        262 CGCACGCCCACGCCGCAGCCCCGCCC---AAGATGGCAAAGTCTACATCAACATGCCAGG 318
              |||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        241 CGCACGCCCACGCCGCAGCCCCGCCCAAGAAGATGGCAAAGTCTACATCAACATGCCAGG 300

Qy        319 CAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGACCCTCTCATCCTGGATGGT 378
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGACCCTCTCATCCTGGATGGT 360

Qy        379 GTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTGTAATAAAACAAT 430
              |||||||||||||||||||||| |||||||||||||||||||| ||||||||||
Db        361 GTGTGGTGGCACAGGAACCCCTGCCCCAACTTTTGGATTGTCATAAAACAAT 412
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RESULT 12
CD049497
LOCUS       CD049497                1265 bp    mRNA    linear   EST 09-MAY-2003
DEFINITION  AGENCOURT_13973607 NIH_MGC_172 Homo sapiens cDNA 5', mRNA sequence.
ACCESSION   CD049497
VERSION     CD049497.1  GI:30485493
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1265)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jamie Thompson, University of WI
             cDNA Library Preparation: Gina Zastrow-Hayes
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: NDKM50  row: e  column: 11
            High quality sequence start: 7
            High quality sequence stop: 345.
FEATURES             Location/Qualifiers
     source          1. .1265
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /tissue_type="embryonic stem cell"
                     /lab_host="DH10B TonA"
                     /clone_lib="NIH_MGC_172"
                     /note="Vector: pDONR201; Site_1: attP2; Site_2: attP1;
                     LIBR_PRIMING - oligo dT; METHOD - full-length enriched;
                     Embryonic Stem Cells H1; LIBR PROVIDER - Bradfield"
BASE COUNT      266 a    433 c    246 g    317 t      3 others
ORIGIN

  Query Match             89.2%;  Score 386.2;  DB 14;  Length 1265;
  Best Local Similarity   98.0%;  Pred. No. 9.7e-85;
  Matches  391;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;
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Qy          2 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         25 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 84

Qy         62 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 144

Qy        122 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 204

Qy        182 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 264

Qy        242 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGGCAAAGTC 301
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        265 GTGGGGGCGGTGCTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGGCAAAGTC 324

Qy        302 TACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGACC 361
              |||||||||||||||||||| |||||||||||||||||||||||||||||| ||||||
Db        325 TACATCAACATGCCAGGCATGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCCGACC 384

Qy        362 CTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCC 400
              ||| ||||||| ||||||||||||| |||||||  ||
Db        385 CTCCCATCCTGAATGGTGTGTGGTGGGACAGGAACGTCC 423
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RESULT 13
AA829607/c
LOCUS       AA829607                 410 bp    mRNA    linear   EST 07-APR-1998
DEFINITION  oe50b04.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1415023 3',
            mRNA sequence.
ACCESSION   AA829607
VERSION     AA829607.1  GI:2902706
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 410)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 517   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 398.
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:1415023"
                     /tissue_type="carcinoid"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Lu5"
                     /note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a
                     modified polylinker; 1st strand cDNA was prepared from
                     neuroendocrine lung carcinoid, and was then primed with a
                     Not I - oligo(dT) primer. Double-stranded cDNA was ligated
                     to Eco RI adaptors (Pharmacia), digested with Not I and
```

cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT 96 a 103 c 136 g 75 t
ORIGIN

Query Match 88.9%; Score 385; DB 9; Length 410;
Best Local Similarity 99.3%; Pred. No. 1.4e-84;
Matches 398; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

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Qy         36 GACCCCAGTCCACCATGATCCATCTGGGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGG 95
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        410 GACCCCAGTCCACCATGATCCATCTGGGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGG 351

Qy         96 CTGCAGCTCAGACGACTCCAGGAGAGAGATCATCACTCCCTGCCTTTTACCCTGGCACTT 155
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        350 CTGCAGCTCAGACGACTCCAGGAGAGAGATCATCACTCCCTGCCTTTTACCCTGGCACTT 291

Qy        156 CAGGCTCTTGTTCCGGATGTGGGTCCCTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTG 215
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        290 CAGGCTCTTGTTCCGGATGTGGGTCCCTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTG 231

Qy        216 CTGATGCGGTGGCATCGCTGCTCATCGTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCC 275
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        230 CTGATGCGGTGGCATCGCTGCTCATCGTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCC 171

Qy        276 GCAGCCCCGCCC---AAGATGGCAAAGTCTACATCAACATGCCAGGCAGGGGCTGACCCT 332
               ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||
Db        170 GCAGCCCCGCCCAAGAAGATGGCAAAGTCTACATCAACATGCCAGGCAGGGGCTGACCCT 111

Qy        333 CCTGCAGCTTGGACCTTTGACTTCTGACCCTCTCATCCTGGATGGTGTGTGGTGGCACAG 392
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        110 CCTGCAGCTTGGACCTTTGACTTCTGACCCTCTCATCCTGGATGGTGTGTGGTGGCACAG 51

Qy        393 GAACCCCCGCCCCAACTTTTGGATTGTAATAAAACAATTGA 433
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Db         50 GAACCCCCGCCCCAACTTTTGGATTGTAATAAAACAATTGA 10
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RESULT 14
AA699808/c
LOCUS AA699808 407 bp mRNA linear EST 19-DEC-1997
DEFINITION zj94c05.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462536 3', mRNA sequence.
ACCESSION AA699808
VERSION AA699808.1 GI:2702771
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 407)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
TITLE WashU-NCI human EST Project
JOURNAL Unpublished
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40m13 fwd. ET from Amersham.
FEATURES Location/Qualifiers
source 1. .407
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3753559"
/db_xref="taxon:9606"
/clone="IMAGE:462536"
/sex="male"
/dev_stage="20 week-post conception fetus"
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/clone_lib="Soares_fetal_liver_spleen_1NFLS_S1"
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Pac I; Site_2: Eco RI; This is a subtracted version of the original Soares fetal liver spleen 1NFLS library. 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 96 a 102 c 136 g 73 t
ORIGIN

Query Match 88.7%; Score 384; DB 9; Length 407;
Best Local Similarity 99.2%; Pred. No. 2.4e-84;
Matches 397; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

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Qy         37 ACCCCAGTCCACCATGATCCATCTGGGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGC 96
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        407 ACCCCAGTCCACCATGATCCATCTGGGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGC 348

Qy         97 TGCAGCTCAGACGACTCCAGGAGAGAGATCATCACTCCCTGCCTTTTACCCTGGCACTTC 156
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        347 TGCAGCTCAGACGACTCCAGGAGAGAGATCATCACTCCCTGCCTTTTACCCTGGCACTTC 288

Qy        157 AGGCTCTTGTTCCGGATGTGGGTCCCTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGC 216
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        287 AGGCTCTTGTTCCGGATGTGGGTCCCTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGC 228

Qy        217 TGATGCGGTGGCATCGCTGCTCATCGTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCG 276
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Db        227 TGATGCGGTGGCATCGCTGCTCATCGTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCG 168

Qy        277 CAGCCCCGCCC---AAGATGGCAAAGTCTACATCAACATGCCAGGCAGGGGCTGACCCTC 333
              ||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||
Db        167 CAGCCCCGCCCAAGAAGATGGCAAAGTCTACATCAACATGCCAGGCAGGGGCTGACCCTC 108

Qy        334 CTGCAGCTTGGACCTTTGACTTCTGACCCTCTCATCCTGGATGGTGTGTGGTGGCACAGG 393
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Db        107 CTGCAGCTTGGACCTTTGACTTCTGACCCTCTCATCCTGGATGGTGTGTGGTGGCACAGG 48

Qy        394 AACCCCCGCCCCAACTTTTGGATTGTAATAAAACAATTGA 433
              |||||||||||||||||||||||||||||||||||||||
Db         47 AACCCCCGCCCCAACTTTTGGATTGTAATAAAACAATTGA 8
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RESULT 15
AA894359/c
LOCUS AA894359 407 bp mRNA linear EST 19-MAY-1998
DEFINITION oj16h09.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1492385 3', mRNA sequence.
ACCESSION AA894359
VERSION AA894359.1 GI:3030760
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 407)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 549 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 383.

FEATURES Location/Qualifiers
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/mol_type="mRNA"
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/clone="IMAGE:1492385"
/tissue_type="2 pooled tumors (clear cell type)"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Kid5"
/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' AACTGGAAGAATTCGCGGCCGCAATATTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT 96 a 102 c 135 g 74 t
ORIGIN

Query Match 88.2%; Score 382; DB 9; Length 407;
Best Local Similarity 99.2%; Pred. No. 7.5e-84;
Matches 395; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

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Qy         39 CCCAGTCCACCATGATCCATCTGGGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTG 98
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        407 CCCAGTCCACCATGATCCATCTGGGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTG 348

Qy         99 CAGCTCAGACGACTCCAGGAGAGAGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAG 158
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        347 CAGCTCAGACGACTCCAGGAGAGAGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAG 288

Qy        159 GCTCTTGTTCCGGATGTGGGTCCCTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTG 218
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        287 GCTCTTGTTCCGGATGTGGGTCCCTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTG 228

Qy        219 ATGCGGTGGCATCGCTGCTCATCGTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCA 278
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        227 ATGCGGTGGCATCGCTGCTCATCGTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCA 168

Qy        279 GCCCCGCCC---AAGATGGCAAAGTCTACATCAACATGCCAGGCAGGGGCTGACCCTCCT 335
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        167 GCCCCGCCCAAGAAGATGGCAAAGTCTACATCAACATGCCAGGCAGGGGCTGACCCTCCT 108

Qy        336 GCAGCTTGGACCTTTGACTTCTGACCCTCTCATCCTGGATGGTGTGTGGTGGCACAGGAA 395
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        107 GCAGCTTGGACCTTTGACTTCTGACCCTCTCATCCTGGATGGTGTGTGGTGGCACAGGAA 48

Qy        396 CCCCCGCCCCAACTTTTGGATTGTAATAAAACAATTGA 433
              |||||||||||||||||||||||||||||||||||||
Db         47 CCCCCGCCCCAACTTTTGGATTGTAATAAAACAATTGA 10
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Search completed: January 29, 2004, 12:50:32
Job time : 1714.35 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 29, 2004, 08:02:48 ; Search time 221.691 Seconds
(without alignments)
5272.456 Million cell updates/sec

Title: US-09-982-405-1
Perfect score: 433
Sequence: 1 gctctggaccacagtcctct.....gattgtaataaaacaattga 433

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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8: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	433	100.0	433	25	ABX11764	cDNA encoding huma
2	432	99.8	446	22	AAS46147	Human DNA encoding
3	432	99.8	446	22	AAC91480	Human PRO1157 cDNA
4	432	99.8	446	22	AAC91562	Human PRO1157 cDNA
5	432	99.8	446	25	ACA57905	Human PRO1157 cDNA
6	432	99.8	446	25	ACA57999	cDNA encoding huma
7	432	99.8	446	25	ABX98375	Human cDNA encodin
8	432	99.8	446	25	ABX98877	Novel human secret
9	432	99.8	446	25	ACA05922	Human secreted/tra
10	432	99.8	446	25	ABX97966	Human PRO polynucl
11	432	99.8	446	25	ABX78750	Human PRO polynucl
12	432	99.8	446	25	ABX75763	Human cDNA encodin
13	432	99.8	446	25	ABX76968	Human PRO polynucl
14	432	99.8	446	25	ABX16808	Human cDNA encodin
15	432	99.8	553	19	AAV34276	Human secreted pro
c 16	419	96.8	456	22	ABA08869	Human membrane pro
17	419	96.8	458	21	AAA62034	Hydrophobic domain
18	419	96.8	506	20	AAZ40811	Secreted protein E
19	419	96.8	518	21	AAZ98140	Human signal pepti
20	419	96.8	532	21	AAA27129	Human inflammation
21	419	96.8	557	19	AAV34223	Human secreted pro
22	419	96.8	753	24	ABS70431	Human bone remodel
23	416.8	96.3	451	20	AAX24396	Human DNAX accesso
24	404	93.3	521	21	AAA52607	Eosinophil activat
25	263	60.7	279	21	AAA62024	Hydrophobic domain
26	213	49.2	231	20	AAX40828	Human secreted pro
27	181.8	42.0	276	25	ABX11765	Degenerate DNA seq
28	109.4	25.3	403	20	AAX24397	Mouse DNAX accesso
29	60	13.9	60	24	ABN35223	Human spliced tran
30	37.4	8.6	1509	25	ABX56070	M. echinospora cal
c 31	36.6	8.5	4403765	22	AAI99683	Mycobacterium tube
c 32	36.6	8.5	4411529	22	AAI99682	Mycobacterium tube
33	36.4	8.4	215	21	AAA45256	Human secreted exp
34	36.4	8.4	2389	21	AAC61893	cDNA encoding a hu
35	36.4	8.4	2755	22	AAS28614	Genomic sequence #
36	36.4	8.4	27148	22	AAS28612	Genomic sequence #
37	36.4	8.4	49634	24	ABL68647	Kidney cancer rela
c 38	36	8.3	50	22	AAL34641	Human SNP oligonuc
39	35.8	8.3	303	25	ABX88728	Corn ear-derived p
c 40	35.6	8.2	10732	21	AAA10594	Gene encoding a su
c 41	35.2	8.1	501	24	ABN24658	Human ORFX polynuc
42	35	8.1	2439	22	AAI65508	Nucleotide sequenc
43	35	8.1	2439	24	AAS20545	Human uroplakin II
c 44	35	8.1	6303	23	AAS86347	DNA encoding novel
45	35	8.1	31024	25	ABV75372	Human IGFBP-2 gene

ALIGNMENTS

RESULT 1
ABX11764
ID ABX11764 standard; cDNA; 433 BP.
XX
AC ABX11764;
XX
DT 10-MAY-2003 (first entry)
XX
DE cDNA encoding human Zsig16.
XX
KW Human; transmembrane protein; Zsig16; peripheral blood lymphocyte;
KW lymphocyte marker; lymphocyte cell type; cancerous cell;
KW chromosome 19q13.12-19q13.2; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 50..325
FT /*tag= a
FT /product= "Zsig16"
FT misc_feature 104..190
FT /*tag= b
FT /note= "Specifically claimed in Claim 9"
FT misc_feature 104..325
FT /*tag= c
FT /note= "Specifically claimed in Claim 10"
XX
PN US2002164764-A1.
XX
PD 07-NOV-2002.
XX

```
PF   18-OCT-2001; 2001US-0982405.
XX
PR   17-SEP-1998;   98US-100865P.
PR   13-SEP-1999;   99US-0394767.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Sheppard PO,  Haldeman BA,  Holly RD;
XX
DR   WPI; 2003-298699/29.
DR   P-PSDB; ABG76299.
XX
PT   New Zsig16 polypeptides, useful in immunological diagnostic assays for
PT   Zsig16 gene expression -
XX
PS   Claim 7; Page 2-3; 30pp; English.
XX
CC   The present invention relates to the isolation of a novel human
CC   transmembrane protein designated Zsig16, and the polynucleotide
CC   sequence encoding it. Zsig16 is expressed by human peripheral blood
CC   lymphocytes. It may be used as a lymphocyte "marker" to distinguish
CC   between normal lymphocyte cell types as well as between normal and
CC   cancerous cells. The Zsig16 polypeptide is useful in diagnosis,
CC   prognosis, and therapy. The present sequence encodes human Zsig16.
CC   The gene encoding Zsig16 is located on chromosome 19q13.12-19q13.2.
XX
SQ   Sequence 433 BP; 73 A; 149 C; 109 G; 102 T; 0 other;

  Query Match             100.0%;  Score 433;  DB 25;  Length 433;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-111;
  Matches  433;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCT 60

Qy         61 GGGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGA 120

Qy        121 GAGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTC 180
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Db        121 GAGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTC 180

Qy        181 CCTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCAT 240

Qy        241 CGTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGGCAAAGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGGCAAAGT 300

Qy        301 CTACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGAC 360

Qy        361 CCTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTGTA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CCTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTGTA 420

Qy        421 ATAAAACAATTGA 433
              |||||||||||||
Db        421 ATAAAACAATTGA 433


RESULT 2
AAS46147
ID   AAS46147 standard; cDNA; 446 BP.
XX
AC   AAS46147;
XX
DT   18-DEC-2001  (first entry)
XX
DE   Human DNA encoding PRO polypeptide sequence #223.
XX
KW   PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss;
KW   dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW   blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW   adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;
KW   PCR primer.
XX
OS   Homo sapiens.
XX
PN   WO200168848-A2.
XX
PD   20-SEP-2001.
XX
PF   28-FEB-2001; 2001WO-US06520.
XX
PR   01-MAR-2000; 2000WO-US05601.
PR   02-MAR-2000; 2000WO-US05841.
PR   03-MAR-2000; 2000US-187202P.
PR   06-MAR-2000; 2000US-186968P.
PR   14-MAR-2000; 2000US-189320P.
PR   14-MAR-2000; 2000US-189328P.
PR   15-MAR-2000; 2000WO-US06884.
PR   21-MAR-2000; 2000US-190828P.
PR   21-MAR-2000; 2000US-191007P.
PR   21-MAR-2000; 2000US-191048P.
PR   21-MAR-2000; 2000US-191314P.
PR   28-MAR-2000; 2000US-192655P.
PR   29-MAR-2000; 2000US-193032P.
PR   29-MAR-2000; 2000US-193053P.
PR   30-MAR-2000; 2000WO-US08439.
PR   04-APR-2000; 2000US-194449P.
PR   04-APR-2000; 2000US-194647P.
PR   11-APR-2000; 2000US-195975P.
PR   11-APR-2000; 2000US-196000P.
PR   11-APR-2000; 2000US-196187P.
PR   11-APR-2000; 2000US-196690P.
PR   11-APR-2000; 2000US-196820P.
PR   18-APR-2000; 2000US-198121P.
PR   18-APR-2000; 2000US-198585P.
PR   25-APR-2000; 2000US-199397P.
PR   25-APR-2000; 2000US-199550P.
PR   25-APR-2000; 2000US-199654P.
PR   03-MAY-2000; 2000US-201516P.
PR   17-MAY-2000; 2000WO-US13705.
PR   22-MAY-2000; 2000WO-US14042.
PR   30-MAY-2000; 2000WO-US14941.
PR   02-JUN-2000; 2000WO-US15264.
PR   05-JUN-2000; 2000US-209832P.
PR   28-JUL-2000; 2000WO-US20710.
PR   22-AUG-2000; 2000US-0644848.
PR   24-AUG-2000; 2000WO-US23328.
PR   08-NOV-2000; 2000WO-US30952.
PR   01-DEC-2000; 2000WO-US32678.
PR   20-DEC-2000; 2000WO-US34956.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Chen J,  Desnoyers L,  Goddard A,  Godowski PJ,  Gurney AL;
PI   Pan J,  Smith V,  Watanabe CK,  Wood WI,  Zhang Z;
XX
DR   WPI; 2001-602746/68.
DR   P-PSDB; AAU29246.
XX
PT   Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT   presence of tumours, such as prostate and breast tumours, in mammals and
PT   to screen for modulators of the compounds -
XX
PS   Claim 2; Fig 445; 774pp; English.
XX
CC   Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR
CC   primers for PRO polypeptides of the invention. The sequences of the
CC   invention can be used to detect the presence of a tumour in a mammal by
```

CC comparing the level of expression of a PRO polypeptide in a test sample
CC of cells from the animal and a control sample of normal cells, whereby a
CC higher level of expression in the test sample indicates the presence of a
CC tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep,
CC pigs, goats and rabbits but are preferably human. The polypeptides can be
CC used to stimulate tumour necrosis factor (TNF) alpha release from human
CC blood, when contacted with it. A specific polypeptide can be used to
CC stimulate the proliferation or differentiation of chondrocyte cells. The
CC PRO proteins can be used to determine the presence of tumours and also
CC susceptibility to tumour development, particularly adrenal, lung, colon,
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC can be used for genetic analysis of individuals with genetic disorders.
XX
SQ Sequence 446 BP; 78 A; 153 C; 110 G; 105 T; 0 other;

Query Match 99.8%; Score 432; DB 22; Length 446;
Best Local Similarity 100.0%; Pred. No. 2.4e-111;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          2 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 61
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Db          8 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 67

Qy         62 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         68 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 127

Qy        122 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 181
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Db        128 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 187

Qy        182 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        188 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 247

Qy        242 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGGCAAAGTC 301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        248 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGGCAAAGTC 307

Qy        302 TACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGACC 361
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        308 TACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGACC 367

Qy        362 CTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTGTAA 421
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Db        368 CTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTGTAA 427

Qy        422 TAAAACAATTGA 433
              ||||||||||||
Db        428 TAAAACAATTGA 439
```

RESULT 3
AAC91480
ID AAC91480 standard; cDNA; 446 BP.
XX
AC AAC91480;
XX
DT 21-MAR-2001 (first entry)
XX
DE Human PRO1157 cDNA.
XX
KW Human; PRO; antiinflammatory; dermatological; antiarthritic;
KW antirheumatic; cardiant; antianaemic; immunosuppressive; antithyroid;
KW antidiabetic; nootropic; neuroprotective; hepatotropic; virucide;
KW antiallergic; antiasthmatic; immune related disorder;
KW hepatobiliary disease; autoimmune disease; allergy; ss.
XX
OS Homo sapiens.
XX
PN WO200073452-A2.
XX
PD 07-DEC-2000.
XX
PF 02-JUN-2000; 2000WO-US15264.
XX
PR 02-JUN-1999; 99WO-US12252.
PR 20-JUL-1999; 99US-0144732.
PR 20-JUL-1999; 99US-0144758.
PR 28-JUL-1999; 99US-0146222.
PR 01-SEP-1999; 99WO-US20111.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 29-OCT-1999; 99US-0162506.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28634.
PR 09-DEC-1999; 99US-0170262.
PR 20-DEC-1999; 99WO-US30911.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ, Gurney AL;
PI Hebert C, Henzel W, Kabakoff RC, Shelton DL, Tumas D, Watanabe CK;
PI Wood WI;
XX
DR WPI; 2001-025253/03.
DR P-PSDB; AAB50921.
XX
PT Thirty three nucleic acids encoding PRO polypeptides which are useful
PT in the diagnosis and treatment of immune related disorders, e.g.
PT systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
PT thyroiditis and diabetes mellitus -
XX
PS Claim 48; Fig 39; 218pp; English.
XX
CC The present sequence is one of thirty three nucleic acids encoding PRO
CC polypeptides. The PRO polypeptides, anti-PRO antibodies, agonists and
CC antagonists are useful for treating and diagnosing immune related
CC disorders such as systemic lupus erythematosus, rheumatoid arthritis,
CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
CC anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,
CC immune-mediated renal disease, demyelinating diseases of the central
CC and peripheral nervous systems (such as multiple sclerosis, idiopathic
CC demyelinating polyneuropathy or Guillain-Barre syndrome, and chronic
CC inflammatory demyelinating polyneuropathy), hepatobiliary diseases
CC (such as infectious, autoimmune chronic active hepatitis, primary
CC biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis),
CC inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's
CC disease, autoimmune or immune-mediated skin diseases (such as bullous
CC skin diseases, erythema multiforme, contact dermatitis, psoriasis),
CC allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,
CC food hypersensitivity and urticaria), immunological diseases of the
CC lung (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis
CC and hypersensitivity pneumonitis), transplantation associated diseases
CC including graft rejection and graft-versus-host diseases.
XX
SQ Sequence 446 BP; 78 A; 153 C; 110 G; 105 T; 0 other;

Query Match 99.8%; Score 432; DB 22; Length 446;
Best Local Similarity 100.0%; Pred. No. 2.4e-111;

```
  Matches  432;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          8 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 67

Qy         62 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         68 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 127

Qy        122 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        128 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 187

Qy        182 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        188 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 247

Qy        242 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGGCAAAGTC 301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        248 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGGCAAAGTC 307

Qy        302 TACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGACC 361
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        308 TACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGACC 367

Qy        362 CTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTGTAA 421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        368 CTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTGTAA 427

Qy        422 TAAAACAATTGA 433
              ||||||||||||
Db        428 TAAAACAATTGA 439


RESULT 4
AAC91562
ID   AAC91562 standard; cDNA; 446 BP.
XX
AC   AAC91562;
XX
DT   21-MAR-2001  (first entry)
XX
DE   Human PRO1157 cDNA.
XX
KW   Human; PRO; cytostatic; nootropic; neuroprotective; respiratory general;
KW   antiinflammatory; antiangiogenic; immunosuppressive; immunostimulant;
KW   PRO agonist; cancer; inflammatory disorder; immunological disorder; ss.
XX
OS   Homo sapiens.
XX
PN   WO200073348-A2.
XX
PD   07-DEC-2000.
XX
PF   30-MAY-2000; 2000WO-US14941.
XX
PR   02-JUN-1999;   99WO-US12252.
PR   22-JUN-1999;   99US-0140650.
PR   23-JUN-1999;   99US-0141037.
PR   20-JUL-1999;   99US-0144758.
PR   01-SEP-1999;   99WO-US20111.
PR   08-SEP-1999;   99WO-US20594.
PR   29-OCT-1999;   99US-0162506.
PR   30-NOV-1999;   99WO-US28313.
PR   01-DEC-1999;   99WO-US28634.
PR   02-DEC-1999;   99WO-US28551.
PR   16-DEC-1999;   99WO-US30095.
PR   20-DEC-1999;   99WO-US30999.
PR   06-JAN-2000; 2000WO-US00376.
PR   11-FEB-2000; 2000WO-US03565.
PR   18-FEB-2000; 2000WO-US04341.
PR   18-FEB-2000; 2000WO-US04342.
PR   02-MAR-2000; 2000WO-US05841.
PR   03-MAR-2000; 2000US-0187202.
PR   10-MAR-2000; 2000WO-US06319.
PR   15-MAR-2000; 2000WO-US06884.
PR   30-MAR-2000; 2000WO-US08439.
PR   17-MAY-2000; 2000WO-US13705.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Goddard A,  Gurney AL,  Hebert C,  Henzel W,  Kabakoff RC;
PI   Shelton DL,  Smith V,  Watanabe CK,  Wood WI;
XX
DR   WPI; 2001-016509/02.
DR   P-PSDB; AAB50960.
XX
PT   Twenty eight nucleic acids encoding PRO polypeptides which are useful
PT   for treating various tumors, e.g. breast cancer, and other
PT   inflammatory, angiogenic and immunological disorders -
XX
PS   Claim 20; Fig 19; 188pp; English.
XX
CC   The present sequence is one of twenty eight nucleic acids encoding PRO
CC   polypeptides. The PRO polypeptides and their agonists, including
CC   antibodies, peptides, and small molecule agonists, may be used to treat
CC   various tumours, e.g., cancers such as breast cancer, ovarian cancer,
CC   renal cancer, colorectal cancer, uterine cancer, prostate cancer, lung
CC   cancer, bladder cancer, central nervous system cancer, melanoma or
CC   leukaemia. They are also useful for treating other disorders
CC   such as neuronal, glial, astrocytal, hypothalamic and other glandular,
CC   macrophagal, epithelial, stromal and blastocoelic disorders, and
CC   inflammatory, angiogenic and immunological disorders.
XX
SQ   Sequence 446 BP; 78 A; 153 C; 110 G; 105 T; 0 other;

  Query Match             99.8%;  Score 432;  DB 22;  Length 446;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-111;
  Matches  432;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          8 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 67

Qy         62 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         68 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 127

Qy        122 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        128 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 187

Qy        182 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 241
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Qy        362 CTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTGTAA 421
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Db        368 CTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTGTAA 427

Qy        422 TAAAACAATTGA 433
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Db        428 TAAAACAATTGA 439


RESULT 5
ACA57905
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ID ACA57905 standard; cDNA; 446 BP.
XX
AC ACA57905;
XX
DT 10-JUN-2003 (first entry)
XX
DE Human PRO1157 cDNA.
XX
KW Human; PRO; secreted; transmembrane; cytostatic; TNF-alpha; blood; gene;
KW tumour necrosis factor alpha release; chondrocyte cell; proliferation;
KW differentiation; tumour; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN US2003036143-A1.
XX
PD 20-FEB-2003.
XX
PF 02-JUL-2002; 2002US-0187600.
XX
PR 16-SEP-1998; 98WO-US19330.
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PR 08-MAR-1999; 99WO-US05028.
PR 14-MAY-1999; 99WO-US10733.
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  Best Local Similarity   100.0%;  Pred. No. 2.4e-111;
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Qy        362 CTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTGTAA 421
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Db        368 CTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTGTAA 427

Qy        422 TAAAACAATTGA 433
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Db        428 TAAAACAATTGA 439


RESULT 6
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ID   ACA57999 standard; cDNA; 446 BP.
XX
AC   ACA57999;
XX
DT   09-JUN-2003  (first entry)
XX
DE   cDNA encoding human neoplasia inhibiting PRO polypeptide PRO1157.
XX
KW   Human; ss; gene; tumour; cancer; neoplasia; liver cancer; sarcoma;
KW   breast cancer; ovarian cancer; renal cancer; colorectal cancer; melanoma;
KW   uterine cancer; prostate cancer; lung cancer; bladder cancer; leukaemia;
KW   gastric cancer; pancreatic cancer; vulval cancer; thyroid cancer;
KW   central nervous system cancer; hepatic carcinoma; glioblastoma;
KW   neuronal disorder; glial disorder; astrocytal disorder;
KW   hypothalamic disorder; glandular disorder; macrophagal disorder;
KW   epithelial disorder; stromal disorder; blastocoelic disorder;
KW   inflammatory disorder; angiogenic disorder; immunologic disorder.
XX
OS   Homo sapiens.
XX
PN   US2002192209-A1.
XX
PD   19-DEC-2002.
XX
PF   30-NOV-2001; 2001US-0001054.
XX
PR   10-SEP-1998;   98WO-US18824.
PR   05-JAN-1999;   99WO-US00106.
PR   08-MAR-1999;   99WO-US05028.
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PR   02-JUN-1999;   99WO-US12252.
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PR   08-SEP-1999;   99WO-US20594.
PR   30-NOV-1999;   99WO-US28313.
PR   01-DEC-1999;   99WO-US28634.
PR   02-DEC-1999;   99WO-US28551.
PR   16-DEC-1999;   99WO-US30095.
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PR   06-JAN-2000; 2000WO-US00376.
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PR   18-FEB-2000; 2000WO-US04341.
PR   18-FEB-2000; 2000WO-US04342.
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PR   30-MAR-2000; 2000WO-US08439.
PR   17-MAY-2000; 2000WO-US13705.
PR   22-MAY-2000; 2000WO-US14042.
PR   30-MAY-2000; 2000WO-US14941.
PR   02-JUN-2000; 2000WO-US15264.
PR   11-AUG-2000; 2000WO-US22031.
PR   23-AUG-2000; 2000WO-US23522.
PR   10-NOV-2000; 2000WO-US30873.
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PR 01-DEC-2000; 2000WO-US32678.
PR 28-FEB-2001; 2001WO-US06520.
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PR 25-MAY-2001; 2001WO-US17092.
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XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W, Kabakoff RC;
PI Shelton DL, Smith V, Watanabe CK, Wood WI;
XX
DR WPI; 2003-328851/31.
DR P-PSDB; ABU71425.
XX
PT Novel isolated PRO polypeptides e.g. PRO240, PRO381, PRO540, useful for
PT treating tumor, preferably cancer, or for treating neuronal, glial,
PT hypothalamic, stromal, inflammatory, angiogenic and immunologic
PT disorders -
XX
PS Claim 20; Fig 19; 186pp; English.
XX
CC The invention relates to an isolated secreted and transmembrane
CC polypeptide, designated as PRO polypeptide, PRO polypeptide lacking its
CC associated signal peptide or PRO polypeptide extracellular domain with or
CC without its associated signal peptide. The PRO polypeptide or an antibody
CC binding to it is useful for inhibiting the growth of a tumor cell. A
CC composition containing a PRO polypeptide is useful for inhibiting
CC neoplastic cell growth or for treating a tumour, preferably cancer (such
CC as liver, breast, ovarian, renal, colorectal, uterine, prostate, lung,
CC bladder, gastric, pancreatic, vulval, thyroid, central nervous system
CC cancer, hepatic carcinomas, sarcomas, glioblastomas, melanoma or
CC leukaemia) in a mammal. The PRO polypeptide is useful for identifying its
CC agonists. The PRO polypeptide or an antibody binding to it is useful in
CC the preparation of a medicament for treating a condition which is
CC responsive to the PRO polypeptide or an antibody binding to it. The PRO
CC polypeptide or an antibody binding to it is also useful for treating
CC neuronal, glial, astrocytal, hypothalamic, glandular, macrophagal,
CC epithelial, stromal, blastocoelic, inflammatory, angiogenic and
CC immunologic disorders. The present sequence represents a cDNA encoding a
CC PRO polypeptides of the invention.
XX
SQ Sequence 446 BP; 78 A; 153 C; 110 G; 105 T; 0 other;

Query Match 99.8%; Score 432; DB 25; Length 446;
Best Local Similarity 100.0%; Pred. No. 2.4e-111;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          8 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 67

Qy         62 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 121
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Qy        122 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 181
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Qy        182 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 241
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Qy        242 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGGCAAAGTC 301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        248 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGGCAAAGTC 307

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        362 CTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTGTAA 421
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Qy        422 TAAAACAATTGA 433
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Db        428 TAAAACAATTGA 439
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RESULT 7
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ID ABX98375 standard; cDNA; 446 BP.
XX
AC ABX98375;
XX
DT 19-MAY-2003 (first entry)
XX
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XX
KW Human; ss; gene; PRO; secreted protein; transmembrane protein;
KW cytostatic; antiarthritic; osteopathic; adrenal tumour; lung tumour;

KW colon tumour; breast tumour; prostate tumour; rectal tumour;
KW cervical tumour; liver tumour; TNF-alpha release; arthritis;
KW tumour necrosis factor alpha; chondrocyte cell; bone disorder;
KW cartilage disorder; sports injury.
XX
OS Homo sapiens.
XX
PN US2003036156-A1.
XX
PD 20-FEB-2003.
XX
PF 02-JUL-2002; 2002US-0188767.
XX
PR 16-SEP-1998; 98WO-US19330.
PR 07-OCT-1998; 98WO-US21141.
PR 01-DEC-1998; 98WO-US25108.
PR 08-MAR-1999; 99WO-US05028.
PR 14-MAY-1999; 99WO-US10733.
PR 02-JUN-1999; 99WO-US12252.
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PR 15-SEP-1999; 99WO-US21090.
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KW   gene Therapy; TNF-Agonist-Alpha; chondrocyte stimulator; tumour;
KW   adrenal tumour; lung tumour; colon tumour; breast tumour;
KW   prostate tumour; rectal tumour; cervical tumour; liver tumour;
KW   gene; ss.
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OS   Homo sapiens.
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PF   02-JUL-2002; 2002US-0188769.
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KW   tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KW   tissue typing.
XX
OS   Homo sapiens.
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PN   US2003036162-A1.
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PD   20-FEB-2003.
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PF   12-JUL-2002; 2002US-0194423.
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PR   02-DEC-1999;   99WO-US28551.
PR   30-DEC-1999;   99WO-US31274.
PR   05-JAN-2000; 2000WO-US00219.
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PR   02-MAR-2000; 2000WO-US05841.
PR   15-MAR-2000; 2000WO-US06884.
PR   30-MAR-2000; 2000WO-US08439.
PR   17-MAY-2000; 2000WO-US13705.
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PR   16-AUG-2001; 2001US-0931836.
PR   28-AUG-2001; 2001US-0941992.
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PR   15-JAN-2002; 2002US-0052586.
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PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI   Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX
DR   WPI; 2003-332039/31.
DR   P-PSDB; ABU67628.
XX
PT   New secreted and transmembrane PRO polypeptides and nucleic acids,
PT   useful in gene therapy, in chromosome and gene mapping, as chromosome
PT   markers, in tissue typing, and in chromosome identification -
XX
PS   Claim 2; Fig 445; 706pp; English.
XX
CC   The invention discloses human nucleic acids encoding secreted and
CC   transmembrane (PRO) polypeptides. Also disclosed is an antibody that
CC   specifically binds to the PRO polypeptide, a method for stimulating the
CC   release of tumour necrosis factor alpha (TNF-alpha) from human blood by
CC   contacting the blood a PRO polypeptide, a method for stimulating the
CC   proliferation or differentiation of chondrocyte cells by contacting the
CC   cells with a PRO polypeptide, a method for detecting the presence of a
CC   tumour in a mammal and an oligonucleotide probe derived from any of the
CC   PRO nucleotide sequences. The nucleotide sequences are useful as probes,
CC   in chromosome and gene mapping, in generating antisense RNA and DNA, in
CC   preparing PRO polypeptides by recombinant techniques and in gene therapy
CC   (e.g. for replacement of defective gene). The PRO polypeptides are useful
CC   as molecular weight markers for protein electrophoresis purposes, for
CC   chromosome identification, as chromosome markers, as therapeutic agents,
```

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CC   for stimulating the release of TNF-alpha from human blood, for
CC   stimulating the proliferation or differentiation of chondrocytes and
CC   detecting the presence of a tumour. The PRO polypeptides and nucleic
CC   acids may also be used diagnostically for tissue typing. The sequences
CC   presented in ACA05700-ACA06004 are the cDNAs encoding the PRO
CC   polypeptides of the invention.
XX
SQ   Sequence 446 BP; 78 A; 153 C; 110 G; 105 T; 0 other;

  Query Match             99.8%;  Score 432;  DB 25;  Length 446;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-111;
  Matches  432;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         62 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 121
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Db         68 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 127

Qy        122 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 181
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Qy        242 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGGCAAAGTC 301
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Qy        422 TAAAACAATTGA 433
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Db        428 TAAAACAATTGA 439


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ID   ABX97966 standard; cDNA; 446 BP.
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DT   16-MAY-2003  (first entry)
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DE   Human PRO polynucleotide #223.
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KW   Human; PRO; gene; ss; cytostatic; chromosome mapping; gene mapping;
KW   protein electrophoresis; tumour necrosis factor-alpha; TNF-alpha; blood;
KW   chondrocyte differentiation; chondrocyte proliferation; tumour.
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OS   Homo sapiens.
XX
PN   US2003032102-A1.
XX
PD   13-FEB-2003.
XX
PF   17-JUN-2002; 2002US-0173697.
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RESULT 11
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AC ABX78750;
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DT 15-APR-2003 (first entry)
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DE Human PRO polynucleotide #223.
XX
KW Human; PRO; gene; ss; cytostatic; tumour; cancer; breast; lung; stomach;
KW liver; dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;
KW antibody-dependent enzyme mediated prodrug therapy.
XX
OS Homo sapiens.
XX
PN US2003027272-A1.
XX
PD 06-FEB-2003.
XX
PF 21-JUN-2002; 2002US-0176492.
XX
PR 16-SEP-1998; 98WO-US19330.
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Qy        422 TAAAACAATTGA 433
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RESULT 12
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DT 26-MAR-2003 (first entry)
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KW antiarthritic; vulnerary; tumour necrosis factor-alpha;
KW chondrocyte cell proliferation; chondrocyte cell differentiation;
KW tumour; adrenal tumour; lung tumour; colon tumour; breast tumour;
KW prostate tumour; rectal tumour; cervical tumour; liver tumour;
KW bone disorder; cartilage disorder; arthritis; sports injury.
XX
OS Homo sapiens.
XX
PN US2003022298-A1.
XX
PD 30-JAN-2003.
XX
PF 20-JUN-2002; 2002US-0176913.
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KW   chondrocyte cell; tumour; adrenal tumour; lung; colon; breast; prostate;
KW   kidney; rectum; cervix; liver; bone disorder; cartilage disorder;
KW   arthritis; sports injury; genetic disorder; antiarthritic; vulnerary.
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OS   Homo sapiens.
XX
PN   US2003027280-A1.
XX
PD   06-FEB-2003.
XX
PF   20-JUN-2002; 2002US-0176993.
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PR 28-MAY-1998; 98US-087098P.
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PR 02-SEP-1998; 98US-098821P.
PR 02-SEP-1998; 98US-098843P.
PR 09-SEP-1998; 98US-099602P.
PR 10-SEP-1998; 98US-099741P.
PR 10-SEP-1998; 98US-099754P.
PR 10-SEP-1998; 98US-099763P.

Query Match 99.8%; Score 432; DB 25; Length 446;
Best Local Similarity 100.0%; Pred. No. 2.4e-111;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          2 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 61
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Db          8 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 67

Qy         62 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         68 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 127

Qy        122 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 181
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Db        128 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 187

Qy        182 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        188 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 247

Qy        242 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGGCAAAGTC 301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        362 CTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTGTAA 421
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Qy        422 TAAAACAATTGA 433
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Db        428 TAAAACAATTGA 439
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RESULT 14
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ID ABX16808 standard; cDNA; 446 BP.
XX
AC ABX16808;
XX
DT 03-FEB-2003 (first entry)
XX
DE Human cDNA encoding secreted/transmembrane protein #223.
XX
KW Human; ss; gene; secreted and transmembrane protein; blood;
KW tumour necrosis factor-alpha; chondrocyte cell proliferation;
KW chondrocyte cell differentiation; tumour; adrenal tumour; lung tumour;
KW colon tumour; breast tumour; prostate tumour; rectal tumour;
KW cervical tumour; liver tumour; bone disorder; cartilage disorder;
KW arthritis; sports injury.

XX
OS Homo sapiens.
XX
PN US2002127584-A1.
XX
PD 12-SEP-2002.
XX
PF 15-JAN-2002; 2002US-0052586.
XX
PR 16-SEP-1998; 98WO-US19330.
PR 07-OCT-1998; 98WO-US21141.
PR 01-DEC-1998; 98WO-US25108.
PR 06-JAN-1999; 2000WO-US00219.
PR 08-MAR-1999; 99WO-US05028.
PR 14-MAY-1999; 99WO-US10733.
PR 02-JUN-1999; 99WO-US12252.
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PR 01-MAR-2000; 2000WO-US05601.
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PR 15-MAR-2000; 2000WO-US06884.
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PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
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PR 09-JUL-2001; 2001WO-US21735.
PR 29-AUG-2001; 2001WO-US27099.
PR 18-SEP-1997; 97US-059263P.
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PR 06-MAY-1998; 98US-084414P.
PR 07-MAY-1998; 98US-084639P.
PR 07-MAY-1998; 98US-084640P.
PR 07-MAY-1998; 98US-084643P.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2003-066893/06.
DR P-PSDB; ABU10732.
XX
PT Novel isolated PRO polypeptides e.g., PRO1079, PRO827, PRO791, PRO1131,
PT PRO1316, PRO1183, PRO1343, PRO1760, PRO1567 or PRO4333, useful for
PT stimulating release of tumor necrosis factor-alpha from human blood -
XX
PS Claim 2; Fig 445; 701pp; English.
XX
CC The invention relates to an isolated PRO polypeptide comprising at least
CC 80% sequence identity to the protein sequences appearing as ABU10510-
CC ABU10814 (including a version lacking its associated signal peptide, or
CC an isolated extracellular domain of a PRO polypeptide with or without
CC its associated signal peptide. Also included are the nucleic acids
CC encoding the PRO proteins (being secreted and transmembrane proteins)
CC appearing as ABX16586-ABX16590, PRO expression vectors, host cells,
CC chimaeric PRO fusion proteins, an anti-PRO antibody and a PRO
CC derived oligonucleotide sequence. The PRO polypeptides are useful for
CC stimulating release of tumour necrosis factor-alpha from human blood.
CC The PRO polypeptide PRO6029 is useful for stimulating proliferation or
CC differentiation of chondrocyte cells. The PRO polypeptides as specified
CC in the specification and having differential expression in tumour cells,
CC are useful for detecting presence of tumour in a mammal (such as adrenal
CC tumour, lung tumour, colon tumour, breast tumour, prostate tumour, rectal
CC tumour, cervical tumour or liver tumour. The PRO polypeptide PRO6029 is
CC useful for treating various bone and/or cartilage disorders such as
CC arthritis, and sports injuries. The PRO polypeptides are useful for
CC screening compounds to identify ant/agonists. PRO nucleic acids
CC are useful as hybridisation probes, in chromosome and gene mapping,
CC in the generation of anti-sense RNA and DNA, for the preparation of PRO
CC polypeptides and for generating knock-out animals. The present
CC sequence encodes a PRO polypeptide.
XX
SQ Sequence 446 BP; 78 A; 153 C; 110 G; 105 T; 0 other;

Query Match 99.8%; Score 432; DB 25; Length 446;
Best Local Similarity 100.0%; Pred. No. 2.4e-111;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 61
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 8 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 67

Qy 62 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 121
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Db 68 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 127

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Qy        122 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 181
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Qy        182 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 241
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Qy        242 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGGCAAAGTC 301
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Qy        302 TACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGACC 361
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Qy        422 TAAAACAATTGA 433
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Db        428 TAAAACAATTGA 439
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RESULT 15
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ID AAV34276 standard; DNA; 553 BP.
XX
AC AAV34276;
XX
DT 25-MAR-2003 (updated)
DT 28-JAN-1999 (first entry)
XX
DE Human secreted protein gene.
XX
KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
OS Homo sapiens.
XX
PN WO9839446-A2.
XX
PD 11-SEP-1998.
XX
PF 06-MAR-1998; 98WO-US04482.
XX
PR 07-MAR-1997; 97US-0038621.
PR 07-MAR-1997; 97US-0040161.
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PR 23-MAY-1997; 97US-0047601.
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PR 23-MAY-1997; 97US-0047618.
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PR 06-JUN-1997; 97US-0048974.
PR 22-AUG-1997; 97US-0056630.
PR 22-AUG-1997; 97US-0056631.
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PR 22-AUG-1997; 97US-0056662.
PR 22-AUG-1997; 97US-0056664.
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PR 22-AUG-1997; 97US-0056903.
PR 22-AUG-1997; 97US-0056908.
PR 22-AUG-1997; 97US-0056909.
PR 22-AUG-1997; 97US-0056910.
PR 22-AUG-1997; 97US-0056911.
PR 05-SEP-1997; 97US-0057650.

PR 05-SEP-1997; 97US-0057761.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Rosen CA, Fischer CL, Soppet DR, Carter KC, Bednarik DP;
PI Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Ferrie AM;
PI Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;
PI Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
XX
DR WPI; 1998-609887/51.
DR P-PSDB; AAW75179.
XX
PT New isolated human genes and the secreted polypeptides they encode
PT - useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders
XX
PS Claim 1; Page 278; 447pp; English.
XX
CC This sequence represents a nucleic acid molecule which encodes a
CC secreted human protein. The gene number, and the clone it is derived
CC from, are detailed in the descriptor line. The gene can be used to
CC generate fusion proteins by linking to the gene to a human immunoglobulin
CC Fc portion (e.g. AAV34145) for increasing the stability of the fused
CC protein as compared to the human protein only.
CC The invention relates to 70 novel genes and their fragments (nucleic
CC acid sequences: AAV34154-V34276; amino acid sequences AAW75057-W75179)
CC which are useful for preventing, treating or ameliorating medical
CC conditions e.g. by protein or gene therapy. Also, pathological
CC conditions can be diagnosed by determining the amount of the new
CC polypeptides in a sample or by determining the presence of mutations in
CC the new polynucleotides. Specific uses are described for each of the 70
CC polynucleotides, based on which tissues they are most highly expressed in
CC (see AAV34154 for described uses).
CC (Updated on 25-MAR-2003 to correct PF field.)
CC (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 553 BP; 124 A; 179 C; 128 G; 122 T; 0 other;

Query Match 99.8%; Score 432; DB 19; Length 553;
Best Local Similarity 100.0%; Pred. No. 2.5e-111;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          2 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 61
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Db         84 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 143

Qy         62 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 121
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Db        144 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 203

Qy        122 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 181
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Qy        182 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 323

Qy        242 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGGCAAAGTC 301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGGCAAAGTC 383

Qy        302 TACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGACC 361
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 TACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGACC 443

Qy        362 CTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTGTAA 421
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Qy        422 TAAAACAATTGA 433
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Db        504 TAAAACAATTGA 515
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Job time : 228.691 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 29, 2004, 12:04:00 ; Search time 266.884 Seconds
(without alignments)
5913.022 Million cell updates/sec

Title: US-09-982-405-1
Perfect score: 433
Sequence: 1 gctctggaccacagtcctct.....gattgtaataaaacaattga 433

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2434939 seqs, 1822278265 residues

Total number of hits satisfying chosen parameters: 4869878

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	433	100.0	433	10	US-09-982-405-1	Sequence 1, Appli
2	432	99.8	446	13	US-10-199-672-445	Sequence 445, App
3	432	99.8	446	13	US-10-187-749-445	Sequence 445, App
4	432	99.8	446	13	US-10-194-457-445	Sequence 445, App
5	432	99.8	446	13	US-10-184-642-445	Sequence 445, App
6	432	99.8	446	13	US-10-196-747-445	Sequence 445, App
7	432	99.8	446	13	US-10-173-689-445	Sequence 445, App
8	432	99.8	446	13	US-10-173-690-445	Sequence 445, App
9	432	99.8	446	13	US-10-173-691-445	Sequence 445, App
10	432	99.8	446	13	US-10-173-692-445	Sequence 445, App
11	432	99.8	446	13	US-10-173-694-445	Sequence 445, App
12	432	99.8	446	13	US-10-173-698-445	Sequence 445, App
13	432	99.8	446	13	US-10-173-699-445	Sequence 445, App
14	432	99.8	446	13	US-10-173-707-445	Sequence 445, App
15	432	99.8	446	13	US-10-174-569-445	Sequence 445, App
16	432	99.8	446	13	US-10-174-583-445	Sequence 445, App
17	432	99.8	446	13	US-10-174-587-445	Sequence 445, App
18	432	99.8	446	13	US-10-174-589-445	Sequence 445, App
19	432	99.8	446	13	US-10-174-591-445	Sequence 445, App
20	432	99.8	446	13	US-10-175-736-445	Sequence 445, App
21	432	99.8	446	13	US-10-175-742-445	Sequence 445, App
22	432	99.8	446	13	US-10-175-744-445	Sequence 445, App
23	432	99.8	446	13	US-10-175-745-445	Sequence 445, App
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25	432	99.8	446	13	US-10-175-751-445	Sequence 445, App
26	432	99.8	446	13	US-10-175-754-445	Sequence 445, App
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31	432	99.8	446	13	US-10-176-759-445	Sequence 445, App
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33	432	99.8	446	13	US-10-176-922-445	Sequence 445, App
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35	432	99.8	446	13	US-10-176-984-445	Sequence 445, App
36	432	99.8	446	13	US-10-179-508-445	Sequence 445, App
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39	432	99.8	446	13	US-10-173-702-445	Sequence 445, App
40	432	99.8	446	13	US-10-173-703-445	Sequence 445, App
41	432	99.8	446	13	US-10-173-704-445	Sequence 445, App
42	432	99.8	446	13	US-10-174-574-445	Sequence 445, App
43	432	99.8	446	13	US-10-176-486-445	Sequence 445, App
44	432	99.8	446	13	US-10-176-490-445	Sequence 445, App
45	432	99.8	446	13	US-10-176-752-445	Sequence 445, App

ALIGNMENTS

RESULT 1
US-09-982-405-1
; Sequence 1, Application US/09982405
; Patent No. US20020164764A1
; GENERAL INFORMATION:
; APPLICANT: Paul O. Sheppard
; APPLICANT: Betty A. Haldeman
; APPLICANT: Richard D. Holly
; TITLE OF INVENTION: Transmembrane Polypeptide Expressed by
; TITLE OF INVENTION: Lymphocytes
; FILE REFERENCE: 98-43C1
; CURRENT APPLICATION NUMBER: US/09/982,405
; CURRENT FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 09/631,073
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 09/394,767
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: 60/100,865
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 433
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (50)...(325)
US-09-982-405-1

Query Match 100.0%; Score 433; DB 10; Length 433;
Best Local Similarity 100.0%; Pred. No. 1.2e-125;
Matches 433; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCT 60
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Db 1 GCTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCT 60

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Qy         61 GGGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGA 120
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Db         61 GGGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGA 120

Qy        121 GAGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTC 180
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Db        121 GAGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTC 180

Qy        181 CCTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCAT 240
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Qy        241 CGTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGGCAAAGT 300
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Qy        301 CTACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGAC 360
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Db        301 CTACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGAC 360

Qy        361 CCTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTGTA 420
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Qy        421 ATAAAACAATTGA 433
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Db        421 ATAAAACAATTGA 433
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RESULT 2
US-10-199-672-445
; Sequence 445, Application US/10199672
; Publication No. US20030148442A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C1
; CURRENT APPLICATION NUMBER: US/10/199,672
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: US/10/052,586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 445
; LENGTH: 446
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-199-672-445

Query Match 99.8%; Score 432; DB 13; Length 446;
Best Local Similarity 100.0%; Pred. No. 2.6e-125;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          2 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 61
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          8 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 67

Qy         62 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 121
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         68 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 127

Qy        122 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 181
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Db        128 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 187

Qy        182 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 241
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        188 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 247

Qy        242 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGGCAAAGTC 301
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        248 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGGCAAAGTC 307

Qy        302 TACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGACC 361
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Db        308 TACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGACC 367

Qy        362 CTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTGTAA 421
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Qy        422 TAAAACAATTGA 433
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RESULT 3
US-10-187-749-445
; Sequence 445, Application US/10187749
; Publication No. US20030153036A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C1
; CURRENT APPLICATION NUMBER: US/10/187,749
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: US/10/052,586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 445
; LENGTH: 446
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-187-749-445

Query Match 99.8%; Score 432; DB 13; Length 446;
Best Local Similarity 100.0%; Pred. No. 2.6e-125;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          2 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 61
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Db          8 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 67

Qy         62 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         68 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 127

Qy        122 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        128 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 187

Qy        182 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        188 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 247

Qy        242 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGGCAAAGTC 301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        248 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGGCAAAGTC 307

Qy        302 TACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGACC 361
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Db        308 TACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGACC 367

Qy        362 CTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTGTAA 421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        368 CTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTGTAA 427

Qy        422 TAAAACAATTGA 433
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Db        428 TAAAACAATTGA 439
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RESULT 4
US-10-194-457-445
; Sequence 445, Application US/10194457
; Publication No. US20030153037A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C296
; CURRENT APPLICATION NUMBER: US/10/194,457
; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 445
; LENGTH: 446
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-194-457-445

Query Match 99.8%; Score 432; DB 13; Length 446;
Best Local Similarity 100.0%; Pred. No. 2.6e-125;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          2 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          8 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 67

Qy         62 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         68 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 127

Qy        122 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        128 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 187

Qy        182 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        188 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 247

Qy        242 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGGCAAAGTC 301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        248 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGGCAAAGTC 307

Qy        302 TACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGACC 361
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        308 TACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGACC 367

Qy        362 CTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTGTAA 421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        368 CTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTGTAA 427

Qy        422 TAAAACAATTGA 433
              ||||||||||||
Db        428 TAAAACAATTGA 439
```

RESULT 5
US-10-184-642-445
; Sequence 445, Application US/10184642
; Publication No. US20030157635A1
; GENERAL INFORMATION:

```
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C194
;  CURRENT APPLICATION NUMBER: US/10/184,642
;  CURRENT FILING DATE:  2002-06-27
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 445
;   LENGTH: 446
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-184-642-445

  Query Match             99.8%;  Score 432;  DB 13;  Length 446;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-125;
  Matches  432;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          8 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 67

Qy         62 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         68 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 127

Qy        122 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        128 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 187

Qy        182 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        188 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 247

Qy        242 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGGCAAAGTC 301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        248 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGGCAAAGTC 307

Qy        302 TACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGACC 361
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        308 TACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGACC 367

Qy        362 CTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTGTAA 421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        368 CTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTGTAA 427

Qy        422 TAAAACAATTGA 433
              ||||||||||||
Db        428 TAAAACAATTGA 439


RESULT 6
US-10-196-747-445
; Sequence 445, Application US/10196747
; Publication No. US20030162250A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C346
;  CURRENT APPLICATION NUMBER: US/10/196,747
;  CURRENT FILING DATE:  2002-07-16
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 445
;   LENGTH: 446
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-196-747-445

  Query Match             99.8%;  Score 432;  DB 13;  Length 446;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-125;
  Matches  432;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          8 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 67

Qy         62 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         68 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 127

Qy        122 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        128 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 187

Qy        182 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        188 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 247

Qy        242 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGGCAAAGTC 301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        248 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGGCAAAGTC 307

Qy        302 TACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGACC 361
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        308 TACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGACC 367

Qy        362 CTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTGTAA 421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        368 CTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTGTAA 427

Qy        422 TAAAACAATTGA 433
              ||||||||||||
Db        428 TAAAACAATTGA 439


RESULT 7
US-10-173-689-445
; Sequence 445, Application US/10173689
; Publication No. US20030166104A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C10
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; CURRENT APPLICATION NUMBER: US/10/173,689
; CURRENT FILING DATE: 2002-06-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 445
; LENGTH: 446
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-173-689-445

Query Match 99.8%; Score 432; DB 13; Length 446;
Best Local Similarity 100.0%; Pred. No. 2.6e-125;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          2 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          8 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 67

Qy         62 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         68 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 127

Qy        122 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        128 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 187

Qy        182 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        188 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 247

Qy        242 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGGCAAAGTC 301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        248 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGGCAAAGTC 307

Qy        302 TACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGACC 361
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        308 TACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGACC 367

Qy        362 CTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTGTAA 421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        368 CTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTGTAA 427

Qy        422 TAAAACAATTGA 433
              ||||||||||||
Db        428 TAAAACAATTGA 439
```

RESULT 8
US-10-173-690-445
; Sequence 445, Application US/10173690
; Publication No. US20030166105A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C9
; CURRENT APPLICATION NUMBER: US/10/173,690
; CURRENT FILING DATE: 2002-06-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 445
; LENGTH: 446
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-173-690-445

Query Match 99.8%; Score 432; DB 13; Length 446;
Best Local Similarity 100.0%; Pred. No. 2.6e-125;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          2 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          8 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 67

Qy         62 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         68 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 127

Qy        122 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        128 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 187

Qy        182 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        188 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 247

Qy        242 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGGCAAAGTC 301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        248 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGGCAAAGTC 307

Qy        302 TACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGACC 361
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        308 TACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGACC 367

Qy        362 CTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTGTAA 421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        368 CTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTGTAA 427

Qy        422 TAAAACAATTGA 433
              ||||||||||||
Db        428 TAAAACAATTGA 439
```

RESULT 9
US-10-173-691-445
; Sequence 445, Application US/10173691
; Publication No. US20030166106A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C13
; CURRENT APPLICATION NUMBER: US/10/173,691
; CURRENT FILING DATE: 2002-06-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 445
; LENGTH: 446
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-173-691-445

Query Match 99.8%; Score 432; DB 13; Length 446;
Best Local Similarity 100.0%; Pred. No. 2.6e-125;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          2 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          8 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 67

Qy         62 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         68 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 127

Qy        122 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        128 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 187

Qy        182 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        188 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 247

Qy        242 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGGCAAAGTC 301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        248 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGGCAAAGTC 307

Qy        302 TACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGACC 361
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        308 TACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGACC 367

Qy        362 CTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTGTAA 421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        368 CTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTGTAA 427

Qy        422 TAAAACAATTGA 433
              ||||||||||||
Db        428 TAAAACAATTGA 439
```

RESULT 10
US-10-173-692-445
; Sequence 445, Application US/10173692
; Publication No. US20030166188A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C20
; CURRENT APPLICATION NUMBER: US/10/173,692
; CURRENT FILING DATE: 2002-06-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 445
; LENGTH: 446
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-173-692-445

Query Match 99.8%; Score 432; DB 13; Length 446;
Best Local Similarity 100.0%; Pred. No. 2.6e-125;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          2 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          8 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 67

Qy         62 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         68 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 127

Qy        122 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        128 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 187

Qy        182 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        188 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 247

Qy        242 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGGCAAAGTC 301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        248 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGGCAAAGTC 307

Qy        302 TACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGACC 361
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        308 TACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGACC 367

Qy        362 CTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTGTAA 421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        368 CTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTGTAA 427

Qy        422 TAAAACAATTGA 433
              ||||||||||||
Db        428 TAAAACAATTGA 439
```

RESULT 11
US-10-173-694-445
; Sequence 445, Application US/10173694
; Publication No. US20030166107A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C19
; CURRENT APPLICATION NUMBER: US/10/173,694
; CURRENT FILING DATE: 2002-06-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 445
; LENGTH: 446
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-173-694-445

Query Match 99.8%; Score 432; DB 13; Length 446;
Best Local Similarity 100.0%; Pred. No. 2.6e-125;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          2 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 61
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Db          8 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 67

Qy         62 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 121
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Db         68 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 127

Qy        122 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        128 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 187

Qy        182 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 241
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Db        188 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 247

Qy        242 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGGCAAAGTC 301
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Db        248 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGGCAAAGTC 307

Qy        302 TACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGACC 361
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Db        308 TACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGACC 367

Qy        362 CTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTGTAA 421
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Db        368 CTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTGTAA 427

Qy        422 TAAAACAATTGA 433
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Db        428 TAAAACAATTGA 439
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RESULT 12
US-10-173-698-445
; Sequence 445, Application US/10173698
; Publication No. US20030166108A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C12
; CURRENT APPLICATION NUMBER: US/10/173,698
; CURRENT FILING DATE: 2002-06-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 445
; LENGTH: 446
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-173-698-445

Query Match 99.8%; Score 432; DB 13; Length 446;
Best Local Similarity 100.0%; Pred. No. 2.6e-125;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          2 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 61
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          8 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 67

Qy         62 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         68 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 127

Qy        122 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        128 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 187

Qy        182 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 241
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Db        188 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 247

Qy        242 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGGCAAAGTC 301
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Db        248 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGGCAAAGTC 307

Qy        302 TACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGACC 361
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        308 TACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGACC 367

Qy        362 CTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTGTAA 421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        368 CTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTGTAA 427

Qy        422 TAAAACAATTGA 433
              ||||||||||||
Db        428 TAAAACAATTGA 439
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RESULT 13
US-10-173-699-445
; Sequence 445, Application US/10173699
; Publication No. US20030166109A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C8
; CURRENT APPLICATION NUMBER: US/10/173,699
; CURRENT FILING DATE: 2002-06-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 445
; LENGTH: 446
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-173-699-445

Query Match 99.8%; Score 432; DB 13; Length 446;
Best Local Similarity 100.0%; Pred. No. 2.6e-125;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          2 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 61
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          8 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 67

Qy         62 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         68 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 127

Qy        122 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 181
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Db        128 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 187

Qy        182 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 241
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Db        188 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 247

Qy        242 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGGCAAAGTC 301
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Db        248 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGGCAAAGTC 307

Qy        302 TACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGACC 361
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Db        308 TACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGACC 367

Qy        362 CTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTGTAA 421
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Db        368 CTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTGTAA 427
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Qy        422 TAAAACAATTGA 433
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Db        428 TAAAACAATTGA 439
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RESULT 14
US-10-173-707-445
; Sequence 445, Application US/10173707
; Publication No. US20030166110A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C17
; CURRENT APPLICATION NUMBER: US/10/173,707
; CURRENT FILING DATE: 2002-06-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 445
; LENGTH: 446
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-173-707-445

Query Match 99.8%; Score 432; DB 13; Length 446;
Best Local Similarity 100.0%; Pred. No. 2.6e-125;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          2 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 61
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Db          8 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 67

Qy         62 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 121
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Db         68 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 127

Qy        122 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 181
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Qy        182 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 241
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Qy        242 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGGCAAAGTC 301
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Db        248 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGGCAAAGTC 307

Qy        302 TACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGACC 361
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Db        308 TACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGACC 367

Qy        362 CTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTGTAA 421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        368 CTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTGTAA 427

Qy        422 TAAAACAATTGA 433
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Db        428 TAAAACAATTGA 439
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RESULT 15
US-10-174-569-445
; Sequence 445, Application US/10174569
; Publication No. US20030166111A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C39
; CURRENT APPLICATION NUMBER: US/10/174,569
; CURRENT FILING DATE: 2002-06-18
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 445
; LENGTH: 446
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-174-569-445

Query Match 99.8%; Score 432; DB 13; Length 446;
Best Local Similarity 100.0%; Pred. No. 2.6e-125;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          2 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 61
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Db          8 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 67

Qy         62 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 121
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Qy        122 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        128 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 187

Qy        182 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        188 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 247

Qy        242 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGGCAAAGTC 301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        248 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGGCAAAGTC 307

Qy        302 TACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGACC 361
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        308 TACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGACC 367

Qy        362 CTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTGTAA 421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        368 CTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTGTAA 427

Qy        422 TAAAACAATTGA 433
              ||||||||||||
Db        428 TAAAACAATTGA 439
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Job time : 270.884 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

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Title: US-09-982-405-1
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Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
	1	419	96.8	506	4	US-09-247-155-69	Sequence 69, Appl
	2	419	96.8	753	4	US-09-484-970B-88	Sequence 88, Appl
	3	416.8	96.3	451	4	US-09-127-946-7	Sequence 7, Appli
	4	109.4	25.3	403	4	US-09-127-946-9	Sequence 9, Appli
	5	47.2	10.9	7218	1	US-08-232-463-14	Sequence 14, Appl
c	6	36.8	8.5	495	4	US-09-252-991A-13925	Sequence 13925, A
c	7	36.6	8.5	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c	8	36.6	8.5	4411529	3	US-09-103-840A-1	Sequence 1, Appli
	9	35.8	8.3	303	4	US-09-313-294A-7188	Sequence 7188, Ap
	10	35	8.1	2439	3	US-08-969-317-1	Sequence 1, Appli
c	11	34.6	8.0	2256	4	US-10-020-079-7	Sequence 7, Appli
c	12	34.6	8.0	2295	4	US-10-020-079-5	Sequence 5, Appli
c	13	34.6	8.0	2331	4	US-10-020-079-23	Sequence 23, Appl
c	14	34.6	8.0	2370	4	US-10-020-079-21	Sequence 21, Appl
c	15	34.6	8.0	2517	4	US-10-020-079-39	Sequence 39, Appl
c	16	34.6	8.0	2556	4	US-10-020-079-37	Sequence 37, Appl
c	17	34.6	8.0	2592	4	US-10-020-079-31	Sequence 31, Appl
c	18	34.6	8.0	2595	4	US-10-020-079-3	Sequence 3, Appli
c	19	34.6	8.0	2613	4	US-10-020-079-1	Sequence 1, Appli
c	20	34.6	8.0	2631	4	US-10-020-079-29	Sequence 29, Appl
c	21	34.6	8.0	2670	4	US-10-020-079-19	Sequence 19, Appl
c	22	34.6	8.0	2688	4	US-10-020-079-17	Sequence 17, Appl
c	23	34.6	8.0	2856	4	US-10-020-079-35	Sequence 35, Appl
c	24	34.6	8.0	2874	4	US-10-020-079-33	Sequence 33, Appl
c	25	34.6	8.0	2931	4	US-10-020-079-27	Sequence 27, Appl
c	26	34.6	8.0	2949	4	US-10-020-079-25	Sequence 25, Appl
c	27	33.6	7.8	4031	2	US-08-993-118-1	Sequence 1, Appli
c	28	33.6	7.8	4031	3	US-08-845-528C-1	Sequence 1, Appli
c	29	33.6	7.8	4031	4	US-09-066-281B-1	Sequence 1, Appli
c	30	33.6	7.8	4225	2	US-08-993-118-9	Sequence 9, Appli
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c	34	33.6	7.8	4265	4	US-09-899-651-1	Sequence 1, Appli
	35	33.4	7.7	1433	2	US-08-666-392A-1	Sequence 1, Appli
	36	33.4	7.7	1433	3	US-09-199-926-1	Sequence 1, Appli
	37	32.8	7.6	4403765	3	US-09-103-840A-2	Sequence 2, Appli
	38	32.8	7.6	4411529	3	US-09-103-840A-1	Sequence 1, Appli
	39	32.4	7.5	1239	4	US-09-252-991A-11463	Sequence 11463, A
	40	32.4	7.5	1752	4	US-09-252-991A-11485	Sequence 11485, A
c	41	32.4	7.5	2106	4	US-09-252-991A-11428	Sequence 11428, A
c	42	32.4	7.5	3009	4	US-09-252-991A-11409	Sequence 11409, A
c	43	32.4	7.5	32654	4	US-09-801-191A-3	Sequence 3, Appli
c	44	32.2	7.4	5897	4	US-09-097-319A-26	Sequence 26, Appl
c	45	32.2	7.4	6898	4	US-09-097-319A-27	Sequence 27, Appl

ALIGNMENTS

RESULT 1
US-09-247-155-69
; Sequence 69, Application US/09247155A
; Patent No. 6312922
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: Complementary DNAs
; FILE REFERENCE: GENSET.021A
; CURRENT APPLICATION NUMBER: US/09/247,155A
; CURRENT FILING DATE: 1999-02-09
; EARLIER APPLICATION NUMBER: 60/074,121
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/081,563
; EARLIER FILING DATE: 1998-04-13
; EARLIER APPLICATION NUMBER: 60/096,116
; EARLIER FILING DATE: 1998-08-10
; EARLIER APPLICATION NUMBER: 60/099,273
; EARLIER FILING DATE: 1998-10-04
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: Patent.pm
; SEQ ID NO 69
; LENGTH: 506
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 98..376
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 98..151
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 12.3
; OTHER INFORMATION: seq HILFLLLLPVAAA/QT
; FEATURE:
; NAME/KEY: polyA_signal
; LOCATION: 471..476
; FEATURE:
; NAME/KEY: polyA_site
; LOCATION: 491..506
US-09-247-155-69

Query Match 96.8%; Score 419; DB 4; Length 506;
Best Local Similarity 99.3%; Pred. No. 1.9e-114;
Matches 432; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

Qy 2 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 61
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Db 50 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 109

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Qy         62 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        110 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 169

Qy        122 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        170 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 229

Qy        182 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        230 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 289

Qy        242 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAG---ATGGCAAA 298
              ||||||||||||||||||||||||||||||||||||||||||||||||   ||||||||
Db        290 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGAATATGGCAAA 349

Qy        299 GTCTACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTG 358
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        350 GTCTACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTG 409

Qy        359 ACCCTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTG 418
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        410 ACCCTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTG 469

Qy        419 TAATAAAACAATTGA 433
              |||||||||||||||
Db        470 TAATAAAACAATTGA 484
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RESULT 2
US-09-484-970B-88
; Sequence 88, Application US/09484970B
; Patent No. 6426186
; GENERAL INFORMATION:
; APPLICANT: Jones, Karen A.
; APPLICANT: Volkmuth, Wayne
; APPLICANT: Walker, Michael G.
; TITLE OF INVENTION: BONE REMODELING GENES
; FILE REFERENCE: PB-0014 US
; CURRENT APPLICATION NUMBER: US/09/484,970B
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PERL Program
; SEQ ID NO 88
; LENGTH: 753
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6426186 235464.2CB1
; NAME/KEY: unsure
; LOCATION: 657
; OTHER INFORMATION: a, t, c, g, or other
US-09-484-970B-88

Query Match 96.8%; Score 419; DB 4; Length 753;
Best Local Similarity 99.3%; Pred. No. 2.3e-114;
Matches 432; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

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Qy          2 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 258

Qy         62 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 318

Qy        122 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 378

Qy        182 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 438

Qy        242 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCC---AAGATGGCAAA 298
              ||||||||||||||||||||||||||||||||||||||||||||||   ||||||||||||
Db        439 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGAAGATGGCAAA 498

Qy        299 GTCTACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTG 358
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 GTCTACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTG 558

Qy        359 ACCCTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTG 418
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 ACCCTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTG 618

Qy        419 TAATAAAACAATTGA 433
              |||||||||||||||
Db        619 TAATAAAACAATTGA 633
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RESULT 3
US-09-127-946-7
; Sequence 7, Application US/09127946
; Patent No. 6416973
; GENERAL INFORMATION:
; APPLICANT: Bakker, Alexander B.H.
; APPLICANT: Phillips, Joseph H.
; APPLICANT: Lanier, Lewis L.
; TITLE OF INVENTION: Mammalian Cell Membrane Proteins;
; TITLE OF INVENTION: Related Reagents
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/127,946
; FILING DATE: 31-JUL-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/089,168
; FILING DATE: 12-JUN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/069,692
; FILING DATE: 16-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/069,639
; FILING DATE: 15-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/063,717
; FILING DATE: 29-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/054,430
; FILING DATE: 01-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0763X
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1200
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 base pairs
; TYPE: nucleic acid

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;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  63..338
;     FEATURE:
;       NAME/KEY:  mat_peptide
;       LOCATION:  117..338
US-09-127-946-7

  Query Match             96.3%;  Score 416.8;  DB 4;  Length 451;
  Best Local Similarity   99.3%;  Pred. No. 8.2e-114;
  Matches  429;  Conservative    0;  Mismatches    2;  Indels    1;  Gaps    1;

Qy          2 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         15 CTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTG 74

Qy         62 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         75 GGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAG 134

Qy        122 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        135 AGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCC 194

Qy        182 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        195 CTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATC 254

Qy        242 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGGCAAAGTC 301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        255 GTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGGCAAAGTC 314

Qy        302 TACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGACC 361
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        315 TACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGACC 374

Qy        362 CTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCCAACTTTTGGATTGTAA 421
              |||||||||||||||||||||||| ||||||||| ||||||||||||||||||||||||||
Db        375 CTCTCATCCTGGATGGTGTGTGGT-GCACAGGAAACCCCGCCCCAACTTTTGGATTGTAA 433

Qy        422 TAAAACAATTGA 433
              |||||||| ||||
Db        434 TAAAACATTTGA 445


RESULT 4
US-09-127-946-9
; Sequence 9, Application US/09127946
; Patent No. 6416973
;  GENERAL INFORMATION:
;    APPLICANT:  Bakker, Alexander B.H.
;    APPLICANT:  Phillips, Joseph H.
;    APPLICANT:  Lanier, Lewis L.
;    TITLE OF INVENTION:  Mammalian Cell Membrane Proteins;
;    TITLE OF INVENTION:  Related Reagents
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DNAX Research Institute
;      STREET:  901 California Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/127,946
;      FILING DATE:  31-JUL-1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/089,168
;      FILING DATE:  12-JUN-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/069,692
;      FILING DATE:  16-DEC-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/069,639
;      FILING DATE:  15-DEC-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/063,717
;      FILING DATE:  29-OCT-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/054,430
;      FILING DATE:  01-AUG-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ching, Edwin P.
;      REGISTRATION NUMBER:  34,090
;      REFERENCE/DOCKET NUMBER:  DX0763X
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650)852-9196
;      TELEFAX:  (650)496-1200
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  403 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  109..345
;    FEATURE:
;      NAME/KEY:  mat_peptide
;      LOCATION:  163..345
US-09-127-946-9

  Query Match             25.3%;  Score 109.4;  DB 4;  Length 403;
  Best Local Similarity   70.1%;  Pred. No. 4.5e-23;
  Matches  162;  Conservative    0;  Mismatches   66;  Indels    3;  Gaps    1;

Qy        156 CAGGCTCTTGTTCCGGATGTGGGTCCCTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTG 215
              |||| || || |||||||||||| | || |||||||| |||||||||||||| |||||||
Db        173 CAGGTTCCTGCTCCGGATGTGGGACTCTGTCTCTGCCACTCCTGGCAGGCCTAGTGGCTG 232

Qy        216 CTGATGCGGTGGCATCGCTGCTCATCGTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCC 275
              | ||||||||    || || || || || |||| ||||||  | |||    ||||||| |
Db        233 CAGATGCGGTCATGTCACTCCTAATTGTAGGGGTGGTGTTTGTATGTATGCGCCCACACG 292

Qy        276 GCAGCCCCGCCC---AAGATGGCAAAGTCTACATCAACATGCCAGGCAGGGGCTGACCCT 332
              |||| || ||||   |||||||| | |||||||||||||||||| ||||| ||||||||
Db        293 GCAGGCCTGCCCAAGAAGATGGTAGAGTCTACATCAACATGCCTGGCAGAGGCTGACCAC 352

Qy        333 CCTGCAGCTTGGACCTTTGACTTCTGACCCTCTCATCCTGGATGGTGTGTG 383
                  |    ||  ||  | |    || ||| |     |||  | |||  |
Db        353 GGCACCTTCTGACCCGCTCATCCTGGATCCTGTGGGTTTGGGGTGCGTGGG 403


RESULT 5
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
;  GENERAL INFORMATION:
;    APPLICANT:  DORNER, F.
;    APPLICANT:  SCHEIFLINGER, F.
;    APPLICANT:  FALKNER, F. G.
;    TITLE OF INVENTION:  RECOMBINANT FOWLPOX VIRUS
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  1800 Diagonal Road, Suite 500
```

```
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22313-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/232,463
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/935,313
;      FILING DATE:
;      APPLICATION NUMBER:  EP 91 114 300.6
;      FILING DATE:  26-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  30472/114 IMMU
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)836-9300
;      TELEFAX:  (703)683-4109
;      TELEX:  899149
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7218 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      CLONE:  pTZgpt-F1s
US-08-232-463-14

  Query Match             10.9%;  Score 47.2;  DB 1;  Length 7218;
  Best Local Similarity   1.1%;  Pred. No. 0.00032;
  Matches    4;  Conservative  221;  Mismatches  149;  Indels    0;  Gaps    0;

Qy          1 GCTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCT 60
              | |::   :: :  :::::: ::   ::::: ::   ::::  ::: :: :  ::: :::
Db       1064 GATYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1123

Qy         61 GGGTCACATCCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGA 120
             :: : :::::::::: ::::: :::::  :  :: :  :::   :  ::::
Db       1124 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1183

Qy        121 GAGATCATCACTCCCTGCCTTTTACCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTC 180
             :: :: :::::: :::::: :::::  : ::::   ::::: ::::   : :   ::
Db       1184 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1243

Qy        181 CCTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCAT 240
             ::::::::: :: :::::  :   :::: :  :: ::  : :  :  : :: :: ::: :
Db       1244 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1303

Qy        241 CGTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGGCAAAGT 300
             : :     :  : ::::: : : : : ::: : :: :  :::: :::    :  :    :
Db       1304 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1363

Qy        301 CTACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGAC 360
             :: : ::  : : ::   :     ::  :::::::: :  :::   ::::: :::::  :
Db       1364 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1423

Qy        361 CCTCTCATCCTGGA 374
             :::::: ::::| |
Db       1424 YYYYYYYYYYGTA 1437


RESULT 6
US-09-252-991A-13925/c
; Sequence 13925, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 13925
;   LENGTH: 495
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13925

  Query Match             8.5%;  Score 36.8;  DB 4;  Length 495;
  Best Local Similarity   50.0%;  Pred. No. 0.13;
  Matches   92;  Conservative    0;  Mismatches   92;  Indels    0;  Gaps    0;

Qy         87 TCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAGAGATCATCACTCCCTGCCTTTTACC 146
              | | |||  || | |      |  || ||||  |   |  | | |||| ||| |
Db        210 TTCGAGTCTCTCCGTCCGCACCACCTTCAGGCTCGGCTTGTCCGGCCGCTGCGGTTGAAG 151

Qy        147 CTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCCCTCTCTCTGCCGCTCCTGGCAGGCC 206
              | || || || ||| |   | ||     | | | | ||| | | |   |     |
Db        150 CCGGAACGTCCGGCACGATTCACGATATGGTGGGCGTAGCTCAGTTGGTAGAGCACAGGA 91

Qy        207 TCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATCGTGGGGGCGGTGTTCCTGTGCGCAC 266
              | |||||| ||| ||  |||| ||| | | ||||||      |  | || |  ||||
Db         90 TTGTGGCTCCTGGTGTCGTGGGTTCGATTCCCATCGTCCACCCCATATTTCGAAGCGCCA 31

Qy        267 GCCC 270
              |||
Db         30 GGCC 27


RESULT 7
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
;  APPLICANT: FLEISCHMAN, Robert D.
;  APPLICANT:  WHITE, Owen R.
;  APPLICANT:  FRASER, Claire M.
;  APPLICANT:  VENTER, John C.
;  TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
;  TITLE OF INVENTION:  TUBERCULOSIS
;  FILE REFERENCE: 24366-20007.00
;  CURRENT APPLICATION NUMBER: US/09/103,840A
;  CURRENT FILING DATE:  1998-06-24
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 4403765
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
;   FEATURE:
;   OTHER INFORMATION: CDC 1551
;   OTHER INFORMATION: "n" bases at various positions throughout the sequence
;   OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

  Query Match             8.5%;  Score 36.6;  DB 3;  Length 4403765;
  Best Local Similarity   48.8%;  Pred. No. 5.1;
  Matches   99;  Conservative    0;  Mismatches  104;  Indels    0;  Gaps    0;

Qy        208 CGTGGCTGCTGATGCGGTGGCATCGCTGCTCATCGTGGGGGCGGTGTTCCTGTGCGCACG 267
              || | || |||   || | || |||   | || || || || || |      | |||   ||
Db     799626 CGGGCCTCCTGGGCCGATCGCGTCGACACCCACCGCGGTGGTGGCGGAAAAGCGCAACCG 799567
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Qy        268 CCCACGCCGCAGCCCCGCCCAAGATGGCAAAGTCTACATCAACATGCCAGGCAGGGGCTG 327
              |  |    ||||  ||  |||     || || | ||  |    ||  | ||||   | |
Db     799566 CACCGCCCGCGTCCGGGCCAGCAGTGTCAGATTCGGCCGTCCCAGCGCGGGCATCAGATA 799507

Qy        328 ACCCTCCTGCAGCTTGGACCTTTGACTTCTGACCCTCTCATCCTGGATGGTGTGTGGTGG 387
              ||  ||  |    |||  | |   | || | |    | |||  | |  |
Db     799506 GCCGACCGCCGAGCTGGTGCGTACGCCGTTAACGATGTTGAGCGGGACCGCGCCTACACC 799447

Qy        388 CACAGGAACCCCCGCCCCAACTT 410
              |  ||| |   ||| ||||||
Db     799446 CGAAGGCATTTCCGGCCCAACAT 799424
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RESULT 8
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match 8.5%; Score 36.6; DB 3; Length 4411529;
Best Local Similarity 48.8%; Pred. No. 5.1;
Matches 99; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

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Qy        208 CGTGGCTGCTGATGCGGTGGCATCGCTGCTCATCGTGGGGGCGGTGTTCCTGTGCGCACG 267
              || | || |||   || | || |||   | || || || || || |     | ||   ||
Db     797665 CGGGCCTCCTGGGCCGATCGCGTCGACACCCACCGCGGTGGTGGCGGAAAAGCGCAACCG 797606

Qy        268 CCCACGCCGCAGCCCCGCCCAAGATGGCAAAGTCTACATCAACATGCCAGGCAGGGGCTG 327
              |  |    ||||  ||  |||     || || | ||  |    ||  | ||||   | |
Db     797605 CACCGCCCGCGTCCGGGCCAGCAGTGTCAGATTCGGCCGTCCCAGCGCGGGCATCAGATA 797546

Qy        328 ACCCTCCTGCAGCTTGGACCTTTGACTTCTGACCCTCTCATCCTGGATGGTGTGTGGTGG 387
              ||  ||  |    |||  | |   | || | |    | |||  | |  |
Db     797545 GCCGACCGCCGAGCTGGTGCGTACGCCGTTAACGATGTTGAGCGGGACCGCGCCTACACC 797486

Qy        388 CACAGGAACCCCCGCCCCAACTT 410
              |  ||| |   ||| ||||||
Db     797485 CGAAGGCATTTCCGGCCCAACAT 797463
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RESULT 9
US-09-313-294A-7188
; Sequence 7188, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 7188
; LENGTH: 303
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6476212 700381278H1
US-09-313-294A-7188

Query Match 8.3%; Score 35.8; DB 4; Length 303;
Best Local Similarity 54.1%; Pred. No. 0.21;
Matches 73; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

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Qy        200 GCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATCGTGGGGGCGGTGTTCCTG 259
              ||  || || |    |  | ||| || ||    || |||  |   ||||  | || | ||
Db         81 GCTCGCTTCCTCCTCGTCGTTGCCGTCGCCCTCCTCCTCCGCCCTGGGGATGCGTCCGTG 140

Qy        260 TGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGGCAAAGTCTACATCAACATGCCAGGC 319
                ||    ||   | | |||| |||| |  | ||||| | || ||||  |    | |||
Db        141 CACGAGTACCGCGGGCTCAGCTTCGCCAACAAGGGCAACGACTTCATCCTCCACGCCGGC 200

Qy        320 AGGGGCTGACCCTCC 334
              || |   | | || |
Db        201 AGCGAGGGCCTCTAC 215
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RESULT 10
US-08-969-317-1
; Sequence 1, Application US/08969317
; Patent No. 6277968
; GENERAL INFORMATION:
; APPLICANT: Tung-Tien Sun, Xue-Ru Wu
; TITLE OF INVENTION: Methods of Detecting and Classifying
; TITLE OF INVENTION: Bladder Cancer
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jane Massey Licata, Esq.
; STREET: 66 E. Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM 486
; OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/969,317
; FILING DATE: herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: NYU-0030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 810-1454
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2439
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; ANTI-SENSE: NO
US-08-969-317-1

Query Match 8.1%; Score 35; DB 3; Length 2439;
Best Local Similarity 46.7%; Pred. No. 0.83;
Matches 107; Conservative 0; Mismatches 122; Indels 0; Gaps 0;

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Qy         26 ACCCCTGCCAGACCCCAGTCCACCATGATCCATCTGGGTCACATCCTCTTCCTGCTTTTG 85
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Db        112 ACCTATTCCACCTCCCAGCCCAGCATGGCACCCCTGCTGCCCATCCGGACCTTGCCCTTG 171

Qy         86 CTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAGAGATCATCACTCCCTGCCTTTTAC 145

Db        172 ATCCTGATTCTGCTGGCTCTGCTGTCCCCAGGGGCTGCAGGTCTCTTCCATCTCTGGCAG 231

Qy        146 CCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCCCTCTCTCTGCCGCTCCTGGCAGGC 205

Db        232 GGGTGGGAAGGGGGCTGGGGGCCTGGACAGGGAGCACTGTACCTTCCAGGGCTCTCAAAN 291

Qy        206 CTCGTGGCTGCTGATGCGGTGGCATCGCTGCTCATCGTGGGGGCGGTGT 254

Db        292 ANAGGTCTGGACAGTTGGGAGTCAGGGCTGGTGATGGCAGTGACTGGGT 340
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RESULT 11
US-10-020-079-7/c
; Sequence 7, Application US/10020079
; Patent No. 6579710
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; APPLICANT: Friddle, Carl Johan
; TITLE OF INVENTION: No. 6579710el Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0281-USA
; CURRENT APPLICATION NUMBER: US/10/020,079
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255,103
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 60/289,422
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 2256
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-020-079-7

Query Match 8.0%; Score 34.6; DB 4; Length 2256;
Best Local Similarity 48.7%; Pred. No. 1.1;
Matches 91; Conservative 1; Mismatches 95; Indels 0; Gaps 0;

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Qy        176 GGGTCCCTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTG 235

Db       1928 GGGTCCGACTCTCTCCGTCGAGGGCGGGGTCCCGAGTGCAGGGGTGAGTGGGAAGGGCTG 1869

Qy        236 CTCATCGTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGGC 295

Db       1868 CCAGGCGTGGGGGGCTGTGACGTCTCGGAACGGCCATCGSCCTGGCTCAGCTGGGGTGGC 1809

Qy        296 AAAGTCTACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTT 355

Db       1808 AGGGGCTGGGGCGGCAAATGCTGCAGGTCCTCCTCCGCCAGCGCCTGCATGCTGCGTCCC 1749

Qy        356 CTGACCC 362

Db       1748 CGGGGCC 1742
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RESULT 12
US-10-020-079-5/c
; Sequence 5, Application US/10020079
; Patent No. 6579710
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; APPLICANT: Friddle, Carl Johan
; TITLE OF INVENTION: No. 6579710el Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0281-USA
; CURRENT APPLICATION NUMBER: US/10/020,079
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255,103
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 60/289,422
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2295
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-020-079-5

Query Match 8.0%; Score 34.6; DB 4; Length 2295;
Best Local Similarity 48.7%; Pred. No. 1.1;
Matches 91; Conservative 1; Mismatches 95; Indels 0; Gaps 0;

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Qy        176 GGGTCCCTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTG 235

Db       1967 GGGTCCGACTCTCTCCGTCGAGGGCGGGGTCCCGAGTGCAGGGGTGAGTGGGAAGGGCTG 1908

Qy        236 CTCATCGTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGGC 295

Db       1907 CCAGGCGTGGGGGGCTGTGACGTCTCGGAACGGCCATCGSCCTGGCTCAGCTGGGGTGGC 1848

Qy        296 AAAGTCTACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTT 355

Db       1847 AGGGGCTGGGGCGGCAAATGCTGCAGGTCCTCCTCCGCCAGCGCCTGCATGCTGCGTCCC 1788

Qy        356 CTGACCC 362

Db       1787 CGGGGCC 1781
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RESULT 13
US-10-020-079-23/c
; Sequence 23, Application US/10020079
; Patent No. 6579710
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; APPLICANT: Friddle, Carl Johan
; TITLE OF INVENTION: No. 6579710el Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0281-USA
; CURRENT APPLICATION NUMBER: US/10/020,079
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255,103
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 60/289,422
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 2331
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-020-079-23

Query Match 8.0%; Score 34.6; DB 4; Length 2331;
Best Local Similarity 48.7%; Pred. No. 1.1;
Matches 91; Conservative 1; Mismatches 95; Indels 0; Gaps 0;

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Qy        176 GGGTCCCTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTG 235

Db       1928 GGGTCCGACTCTCTCCGTCGAGGGCGGGGTCCCGAGTGCAGGGGTGAGTGGGAAGGGCTG 1869

Qy        236 CTCATCGTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGGC 295

Db       1868 CCAGGCGTGGGGGGCTGTGACGTCTCGGAACGGCCATCGSCCTGGCTCAGCTGGGGTGGC 1809

Qy        296 AAAGTCTACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTT 355

Db       1808 AGGGGCTGGGGCGGCAAATGCTGCAGGTCCTCCTCCGCCAGCGCCTGCATGCTGCGTCCC 1749
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Qy        356 CTGACCC 362
              | | | ||
Db       1748 CGGGGCC 1742
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RESULT 14
US-10-020-079-21/c
; Sequence 21, Application US/10020079
; Patent No. 6579710
; GENERAL INFORMATION:
;  APPLICANT: Turner, C. Alexander Jr.
;  APPLICANT:  Mathur, Brian
;  APPLICANT:  Friddle, Carl Johan
;  TITLE OF INVENTION: No. 6579710el Human Kinases and Polynucleotides Encoding the Same
;  FILE REFERENCE: LEX-0281-USA
;  CURRENT APPLICATION NUMBER: US/10/020,079
;  CURRENT FILING DATE:  2001-12-12
;  PRIOR APPLICATION NUMBER: US 60/255,103
;  PRIOR FILING DATE: 2000-12-12
;  PRIOR APPLICATION NUMBER: US 60/289,422
;  PRIOR FILING DATE: 2001-05-08
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21
;   LENGTH: 2370
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-10-020-079-21

  Query Match             8.0%;  Score 34.6;  DB 4;  Length 2370;
  Best Local Similarity   48.7%;  Pred. No. 1.1;
  Matches   91;  Conservative    1;  Mismatches   95;  Indels    0;  Gaps    0;

Qy        176 GGGTCCCTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTG 235
              ||||||  ||||||  |  |     |  || | || |       | ||  |  || |  ||||
Db       1967 GGGTCCGACTCTCTCCGTCGAGGGCGGGGTCCCGAGTGCAGGGGTGAGTGGGAAGGGCTG 1908

Qy        236 CTCATCGTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGGC 295
              |    ||||||||        | |  |  | ||| |||   :  | | | |  |   | ||||
Db       1907 CCAGGCGTGGGGGGCTGTGACGTCTCGGAACGGCCATCGSCCTGGCTCAGCTGGGGTGGC 1848

Qy        296 AAAGTCTACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTT 355
              |  | ||    |  ||      |||||  ||   || || ||  ||     ||  | |
Db       1847 AGGGGCTGGGGCGGCAAATGCTGCAGGTCCTCCTCCGCCAGCGCCTGCATGCTGCGTCCC 1788

Qy        356 CTGACCC 362
              | | | ||
Db       1787 CGGGGCC 1781
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RESULT 15
US-10-020-079-39/c
; Sequence 39, Application US/10020079
; Patent No. 6579710
; GENERAL INFORMATION:
;  APPLICANT: Turner, C. Alexander Jr.
;  APPLICANT:  Mathur, Brian
;  APPLICANT:  Friddle, Carl Johan
;  TITLE OF INVENTION: No. 6579710el Human Kinases and Polynucleotides Encoding the Same
;  FILE REFERENCE: LEX-0281-USA
;  CURRENT APPLICATION NUMBER: US/10/020,079
;  CURRENT FILING DATE:  2001-12-12
;  PRIOR APPLICATION NUMBER: US 60/255,103
;  PRIOR FILING DATE: 2000-12-12
;  PRIOR APPLICATION NUMBER: US 60/289,422
;  PRIOR FILING DATE: 2001-05-08
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 39
;   LENGTH: 2517
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-10-020-079-39

  Query Match             8.0%;  Score 34.6;  DB 4;  Length 2517;
  Best Local Similarity   48.7%;  Pred. No. 1.1;
  Matches   91;  Conservative    1;  Mismatches   95;  Indels    0;  Gaps    0;

Qy        176 GGGTCCCTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGATGCGGTGGCATCGCTG 235
              ||||||  ||||||  |  |     |  || | || |       | ||  |  || |  ||||
Db       2189 GGGTCCGACTCTCTCCGTCGAGGGCGGGGTCCCGAGTGCAGGGGTGAGTGGGAAGGGCTG 2130

Qy        236 CTCATCGTGGGGGCGGTGTTCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGGC 295
              |    ||||||||        | |  |  | ||| |||   :  | | | |  |   | ||||
Db       2129 CCAGGCGTGGGGGGCTGTGACGTCTCGGAACGGCCATCGSCCTGGCTCAGCTGGGGTGGC 2070

Qy        296 AAAGTCTACATCAACATGCCAGGCAGGGGCTGACCCTCCTGCAGCTTGGACCTTTGACTT 355
              |  | ||    |  ||      |||||  ||   || || ||  ||     ||  | |
Db       2069 AGGGGCTGGGGCGGCAAATGCTGCAGGTCCTCCTCCGCCAGCGCCTGCATGCTGCGTCCC 2010

Qy        356 CTGACCC 362
              | | | ||
Db       2009 CGGGGCC 2003
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Search completed: January 29, 2004, 12:52:17
Job time : 70.5219 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 29, 2004, 08:42:17 ; Search time 41 Seconds
(without alignments)
356.167 Million cell updates/sec

Title: US-09-982-405-2
Perfect score: 469
Sequence: 1 MIHLGHILFLLLLPVAAAQT.....RPRRSPAQDGKVYINMPGRG 92

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	469	100.0	92	20	AAW97871	Human DNAX accesso
2	469	100.0	92	22	AAU29246	Human PRO polypept
3	469	100.0	92	22	AAB50921	Human PRO1157 prot
4	469	100.0	92	22	AAB50960	Human PRO1157 prot
5	469	100.0	92	24	ABU71334	Human PRO1157 prot
6	469	100.0	92	24	ABU71426	Human neoplasia in
7	469	100.0	92	24	ABU65791	Human secreted/tra
8	469	100.0	92	24	ABU66124	Novel human secret
9	469	100.0	92	24	ABU67628	Human secreted/tra
10	469	100.0	92	24	ABG76299	Amino acid sequenc
11	469	100.0	92	24	ABU65486	Human PRO polypept
12	469	100.0	92	24	ABU58622	Human PRO polypept
13	469	100.0	92	24	ABU56158	Human secreted/tra
14	469	100.0	92	24	ABU57153	Human PRO polypept
15	469	100.0	92	24	ABU10732	Human secreted/tra
16	469	100.0	93	19	AAW75179	Human secreted pro
17	458.5	97.8	93	19	AAW75126	Human secreted pro
18	458.5	97.8	93	21	AAB12141	Hydrophobic domain
19	458.5	97.8	93	21	AAY94448	Human inflammation
20	458.5	97.8	93	21	AAY87255	Human signal pepti
21	458.5	97.8	110	22	ABB11625	Human membrane pro
22	454.5	96.9	93	20	AAY59683	Secreted protein 1
23	285.5	60.9	79	20	AAW97872	Mouse DNAX accesso
24	281	59.9	55	20	AAY11995	Human 5' EST secre
25	163	34.8	30	23	AAU72824	Human DAP10 extrac
26	115	24.5	21	23	AAU72825	Anti-NKG2D hybrido
27	79	16.8	655	22	ABG23459	Novel human diagno
28	78.5	16.7	749	23	AAM52830	Physcomitrella pat
29	76	16.2	124	20	AAW87526	Partial murine KAR
30	75	16.0	2214	18	AAW26357	Human LDL receptor
31	75	16.0	2214	23	ABG96421	Human ovarian canc
32	75	16.0	2214	23	ABB85016	Pain regulated pro
33	75	16.0	2214	24	ABR48181	Human bladder canc
34	75	16.0	2214	24	ABJ37071	Human breast cance
35	75	16.0	2214	24	ABU04144	Human expressed pr
36	75	16.0	2214	24	ABU04145	Human expressed pr
37	75	16.0	2214	24	ABU04146	Human expressed pr
38	75	16.0	2214	24	ABU04147	Human expressed pr
39	75	16.0	2214	24	ABU04148	Human expressed pr
40	74.5	15.9	180	22	AAB90779	Human shear stress
41	74.5	15.9	185	21	AAB58380	Lung cancer associ
42	74	15.8	103	20	AAY12345	Human 5' EST secre
43	74	15.8	426	22	AAG92282	C glutamicum prote
44	74	15.8	426	22	AAB76721	Corynebacterium gl
45	73.5	15.7	113	20	AAW97869	Human DNAX accesso

ALIGNMENTS

RESULT 1
AAW97871
ID AAW97871 standard; Protein; 92 AA.
XX
AC AAW97871;
XX
DT 07-JUN-1999 (first entry)
XX
DE Human DNAX accessory protein, 10 kD (DAP10).
XX
KW DNAX accessory protein 10 kD; DAP10; human; cell signalling;
KW signal transduction; immunomodulator; cancer; therapy.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	Peptide	1..18
FT		/note= "signal peptide. The actual cleavage point may be different from that indicated, e.g. between Ala-27 and Gln-28"
FT	Protein	19..92
FT		/note= "mature protein"
FT	Domain	19..48
FT		/note= "extracellular domain"
FT	Domain	48..68
FT		/note= "transmembrane domain"
FT	Domain	69..92
FT		/note= "cytoplasmic domain"
FT	Peptide	85..88
FT		/note= "YXXM motif, similar to that seen in CD28, CTLA-4 and CD19"
FT	Disulfide-bond	39

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FT                   /note= "putative dusulfide link to homotypic or
FT                          heterotypic accessory proteins"
FT   Disulfide-bond  42
FT                   /note= "putative dusulfide link to homotypic or
FT                          heterotypic accessory proteins"
XX
PN   WO9906557-A2.
XX
PD   11-FEB-1999.
XX
PF   31-JUL-1998;   98WO-US15316.
XX
PR   12-JUN-1998;   98US-0089168.
PR   01-AUG-1997;   97US-0904905.
PR   29-OCT-1997;   97US-0063717.
PR   15-DEC-1997;   97US-0990820.
PR   16-DEC-1997;   97US-0069692.
XX
PA   (SCHE ) SCHERING CORP.
XX
PI   Bakker ABH,  Lanier LL,  Phillips JH;
XX
DR   WPI; 1999-153787/13.
DR   N-PSDB; AAX24396.
XX
PT   New mammalian cell membrane proteins DAP12, DAP10 and MDL-1 - useful
PT   to modulate the physiology and development of cells
XX
PS   Claim 1; Page 124; 131pp; English.
XX
CC   This is the amino acid sequence of novel human DNAX accessory
CC   protein 10 kD (DAP10), a cell surface protein that exhibits
CC   many structural and biological similarities to novel DAP12 (see
CC   AAW97869), but which contains an immunoreceptor tyrosine-based
CC   inhibitor motif (ITIM) rather than an immunoreceptor tyrosine-based
CC   activation motif (ITAM).  The amino acid sequence was deduced from
CC   an isolated cDNA clone (see AAX24396).  The invention provides human
CC   and mouse DAP12, DAP10 and myeloid DAP12 associated lectin-1
CC   (MDL-1) polynucleotides (see AAX24394-99) and polypeptides (see
CC   AAW97869-75).  These can be used to modulate cell development and
CC   physiology, including lymphoid and myeloid cells.  In particular,
CC   they can be used to treat abnormal B cell responses in e.g. cancer.
XX
SQ   Sequence   92 AA;

  Query Match             100.0%;  Score 469;  DB 20;  Length 92;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-43;
  Matches   92;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MIHLGHILFLLLLPVAAAQTTPGERSSLPAFYPGTSGSCSGCGSLSLPLLAGLVAADAVA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MIHLGHILFLLLLPVAAAQTTPGERSSLPAFYPGTSGSCSGCGSLSLPLLAGLVAADAVA 60

Qy         61 SLLIVGAVFLCARPRRSPAQDGKVYINMPGRG 92
              ||||||||||||||||||||||||||||||||
Db         61 SLLIVGAVFLCARPRRSPAQDGKVYINMPGRG 92


RESULT 2
AAU29246
ID   AAU29246 standard; Protein; 92 AA.
XX
AC   AAU29246;
XX
DT   18-DEC-2001  (first entry)
XX
DE   Human PRO polypeptide sequence #223.
XX
KW   PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
KW   dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW   blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW   adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
XX
OS   Homo sapiens.
XX
PN   WO200168848-A2.
XX
PD   20-SEP-2001.
XX
PF   28-FEB-2001; 2001WO-US06520.
XX
PR   01-MAR-2000; 2000WO-US05601.
PR   02-MAR-2000; 2000WO-US05841.
PR   03-MAR-2000; 2000US-187202P.
PR   06-MAR-2000; 2000US-186968P.
PR   14-MAR-2000; 2000US-189320P.
PR   14-MAR-2000; 2000US-189328P.
PR   15-MAR-2000; 2000WO-US06884.
PR   21-MAR-2000; 2000US-190828P.
PR   21-MAR-2000; 2000US-191007P.
PR   21-MAR-2000; 2000US-191048P.
PR   21-MAR-2000; 2000US-191314P.
PR   28-MAR-2000; 2000US-192655P.
PR   29-MAR-2000; 2000US-193032P.
PR   29-MAR-2000; 2000US-193053P.
PR   30-MAR-2000; 2000WO-US08439.
PR   04-APR-2000; 2000US-194449P.
PR   04-APR-2000; 2000US-194647P.
PR   11-APR-2000; 2000US-195975P.
PR   11-APR-2000; 2000US-196000P.
PR   11-APR-2000; 2000US-196187P.
PR   11-APR-2000; 2000US-196690P.
PR   11-APR-2000; 2000US-196820P.
PR   18-APR-2000; 2000US-198121P.
PR   18-APR-2000; 2000US-198585P.
PR   25-APR-2000; 2000US-199397P.
PR   25-APR-2000; 2000US-199550P.
PR   25-APR-2000; 2000US-199654P.
PR   03-MAY-2000; 2000US-201516P.
PR   17-MAY-2000; 2000WO-US13705.
PR   22-MAY-2000; 2000WO-US14042.
PR   30-MAY-2000; 2000WO-US14941.
PR   02-JUN-2000; 2000WO-US15264.
PR   05-JUN-2000; 2000US-209832P.
PR   28-JUL-2000; 2000WO-US20710.
PR   22-AUG-2000; 2000US-0644848.
PR   24-AUG-2000; 2000WO-US23328.
PR   08-NOV-2000; 2000WO-US30952.
PR   01-DEC-2000; 2000WO-US32678.
PR   20-DEC-2000; 2000WO-US34956.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Chen J,  Desnoyers L,  Goddard A,  Godowski PJ,  Gurney AL;
PI   Pan J,  Smith V,  Watanabe CK,  Wood WI,  Zhang Z;
XX
DR   WPI; 2001-602746/68.
DR   N-PSDB; AAS46147.
XX
PT   Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT   presence of tumours, such as prostate and breast tumours, in mammals and
PT   to screen for modulators of the compounds -
XX
PS   Claim 11; Fig 446; 774pp; English.
XX
CC   Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
CC   The PRO polypeptides and their associated nucleic acids can be used to
CC   detect the presence of a tumour in a mammal by comparing the level of
CC   expression of a PRO polypeptide in a test sample of cells from the animal
CC   and a control sample of normal cells, whereby a higher level of
CC   expression in the test sample indicates the presence of a tumour in the
CC   mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
CC   and rabbits but are preferably human. The polypeptides can be used to
CC   stimulate tumour necrosis factor (TNF) alpha release from human blood,
CC   when contacted with it. A specific polypeptide can be used to stimulate
CC   the proliferation or differentiation of chondrocyte cells. The PRO
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CC   proteins can be used to determine the presence of tumours and also
CC   susceptibility to tumour development, particularly adrenal, lung, colon,
CC   breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC   subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC   can be used for genetic analysis of individuals with genetic disorders.
XX
SQ   Sequence   92 AA;

  Query Match             100.0%;  Score 469;  DB 22;  Length 92;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-43;
  Matches   92;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MIHLGHILFLLLLPVAAAQTTPGERSSLPAFYPGTSGSCSGCGSLSLPLLAGLVAADAVA 60
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Db          1 MIHLGHILFLLLLPVAAAQTTPGERSSLPAFYPGTSGSCSGCGSLSLPLLAGLVAADAVA 60

Qy         61 SLLIVGAVFLCARPRRSPAQDGKVYINMPGRG 92
              ||||||||||||||||||||||||||||||||
Db         61 SLLIVGAVFLCARPRRSPAQDGKVYINMPGRG 92


RESULT 3
AAB50921
ID   AAB50921 standard; Protein; 92 AA.
XX
AC   AAB50921;
XX
DT   21-MAR-2001  (first entry)
XX
DE   Human PRO1157 protein.
XX
KW   Human; PRO; antiinflammatory; dermatological; antiarthritic;
KW   antirheumatic; cardiant; antianaemic; immunosuppressive; antithyroid;
KW   antidiabetic; nootropic; neuroprotective; hepatotropic; virucide;
KW   antiallergic; antiasthmatic; immune related disorder;
KW   hepatobiliary disease; autoimmune disease; allergy.
XX
OS   Homo sapiens.
XX
PN   WO200073452-A2.
XX
PD   07-DEC-2000.
XX
PF   02-JUN-2000; 2000WO-US15264.
XX
PR   02-JUN-1999;   99WO-US12252.
PR   20-JUL-1999;   99US-0144732.
PR   20-JUL-1999;   99US-0144758.
PR   28-JUL-1999;   99US-0146222.
PR   01-SEP-1999;   99WO-US20111.
PR   15-SEP-1999;   99WO-US21090.
PR   15-SEP-1999;   99WO-US21547.
PR   29-OCT-1999;   99US-0162506.
PR   30-NOV-1999;   99WO-US28313.
PR   01-DEC-1999;   99WO-US28634.
PR   09-DEC-1999;   99US-0170262.
PR   20-DEC-1999;   99WO-US30911.
PR   05-JAN-2000; 2000WO-US00219.
PR   06-JAN-2000; 2000WO-US00376.
PR   11-FEB-2000; 2000WO-US03565.
PR   18-FEB-2000; 2000WO-US04341.
PR   18-FEB-2000; 2000WO-US04342.
PR   22-FEB-2000; 2000WO-US04414.
PR   24-FEB-2000; 2000WO-US04914.
PR   15-MAR-2000; 2000WO-US06884.
PR   20-MAR-2000; 2000WO-US07377.
PR   21-MAR-2000; 2000WO-US07532.
PR   30-MAR-2000; 2000WO-US08439.
PR   17-MAY-2000; 2000WO-US13705.
PR   22-MAY-2000; 2000WO-US14042.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Chan B,  Goddard A,  Godowski PJ,  Gurney AL;
PI   Hebert C,  Henzel W,  Kabakoff RC,  Shelton DL,  Tumas D,  Watanabe CK;
PI   Wood WI;
XX
DR   WPI; 2001-025253/03.
DR   N-PSDB; AAC91480.
XX
PT   Thirty three nucleic acids encoding PRO polypeptides which are useful
PT   in the diagnosis and treatment of immune related disorders, e.g.
PT   systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
PT   thyroiditis and diabetes mellitus -
XX
PS   Claim 58; Fig 40; 218pp; English.
XX
CC   The present sequence is one of thirty three novel PRO polypeptides.
CC   The PRO polypeptides, anti-PRO antibodies, agonists and
CC   antagonists are useful for treating and diagnosing immune related
CC   disorders such as systemic lupus erythematosus, rheumatoid arthritis,
CC   osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
CC   systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
CC   syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
CC   anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,
CC   immune-mediated renal disease, demyelinating diseases of the central
CC   and peripheral nervous systems (such as multiple sclerosis, idiopathic
CC   demyelinating polyneuropathy or Guillain-Barre syndrome, and chronic
CC   inflammatory demyelinating polyneuropathy), hepatobiliary diseases
CC   (such as infectious, autoimmune chronic active hepatitis, primary
CC   biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis),
CC   inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's
CC   disease, autoimmune or immune-mediated skin diseases (such as bullous
CC   skin diseases, erythema multiforme, contact dermatitis, psoriasis),
CC   allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,
CC   food hypersensitivity and urticaria), immunological diseases of the
CC   lung (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis
CC   and hypersensitivity pneumonitis), transplantation associated diseases
CC   including graft rejection and graft-versus-host diseases.
XX
SQ   Sequence   92 AA;

  Query Match             100.0%;  Score 469;  DB 22;  Length 92;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-43;
  Matches   92;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MIHLGHILFLLLLPVAAAQTTPGERSSLPAFYPGTSGSCSGCGSLSLPLLAGLVAADAVA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MIHLGHILFLLLLPVAAAQTTPGERSSLPAFYPGTSGSCSGCGSLSLPLLAGLVAADAVA 60

Qy         61 SLLIVGAVFLCARPRRSPAQDGKVYINMPGRG 92
              ||||||||||||||||||||||||||||||||
Db         61 SLLIVGAVFLCARPRRSPAQDGKVYINMPGRG 92


RESULT 4
AAB50960
ID   AAB50960 standard; Protein; 92 AA.
XX
AC   AAB50960;
XX
DT   21-MAR-2001  (first entry)
XX
DE   Human PRO1157 protein.
XX
KW   Human; PRO; cytostatic; nootropic; neuroprotective; respiratory general;
KW   antiinflammatory; antiangiogenic; immunosuppressive; immunostimulant;
KW   PRO agonist; cancer; inflammatory disorder; immunological disorder.
XX
OS   Homo sapiens.
XX
PN   WO200073348-A2.
XX
PD   07-DEC-2000.
XX
PF   30-MAY-2000; 2000WO-US14941.
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XX
PR 02-JUN-1999; 99WO-US12252.
PR 22-JUN-1999; 99US-0140650.
PR 23-JUN-1999; 99US-0141037.
PR 20-JUL-1999; 99US-0144758.
PR 01-SEP-1999; 99WO-US20111.
PR 08-SEP-1999; 99WO-US20594.
PR 29-OCT-1999; 99US-0162506.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US28551.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30999.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 02-MAR-2000; 2000WO-US05841.
PR 03-MAR-2000; 2000US-0187202.
PR 10-MAR-2000; 2000WO-US06319.
PR 15-MAR-2000; 2000WO-US06884.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W, Kabakoff RC;
PI Shelton DL, Smith V, Watanabe CK, Wood WI;
XX
DR WPI; 2001-016509/02.
DR N-PSDB; AAC91562.
XX
PT Twenty eight nucleic acids encoding PRO polypeptides which are useful
PT for treating various tumors, e.g. breast cancer, and other
PT inflammatory, angiogenic and immunological disorders -
XX
PS Claim 31; Fig 20; 188pp; English.
XX
CC The present sequence is one of twenty eight novel PRO polypeptides. The
CC PRO polypeptides and their agonists, including antibodies, peptides, and
CC small molecule agonists, may be used to treat various tumours, e.g.,
CC cancers such as breast cancer, ovarian cancer, renal cancer, colorectal
CC cancer, uterine cancer, prostate cancer, lung cancer, bladder cancer,
CC central nervous system cancer, melanoma or leukaemia. They are also
CC useful for treating other disorders such as neuronal, glial, astrocytal,
CC hypothalamic and other glandular, macrophagal, epithelial, stromal and
CC blastocoelic disorders, and inflammatory, angiogenic and immunological
CC disorders.
XX
SQ Sequence 92 AA;

Query Match 100.0%; Score 469; DB 22; Length 92;
Best Local Similarity 100.0%; Pred. No. 1.1e-43;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MIHLGHILFLLLLPVAAAQTTPGERSSLPAFYPGTSGSCSGCGSLSLPLLAGLVAADAVA 60
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Db          1 MIHLGHILFLLLLPVAAAQTTPGERSSLPAFYPGTSGSCSGCGSLSLPLLAGLVAADAVA 60

Qy         61 SLLIVGAVFLCARPRRSPAQDGKVYINMPGRG 92
              ||||||||||||||||||||||||||||||||
Db         61 SLLIVGAVFLCARPRRSPAQDGKVYINMPGRG 92
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RESULT 5
ABU71334
ID ABU71334 standard; Protein; 92 AA.
XX
AC ABU71334;
XX
DT 10-JUN-2003 (first entry)
XX
DE Human PRO1157 protein.
XX
KW Human; PRO; secreted; transmembrane; cytostatic; TNF-alpha; blood;
KW tumour necrosis factor alpha release; chondrocyte cell; proliferation;
KW differentiation; tumour; gene therapy.
XX
OS Homo sapiens.
XX
PN US2003036143-A1.
XX
PD 20-FEB-2003.
XX
PF 02-JUL-2002; 2002US-0187600.
XX
PR 16-SEP-1998; 98WO-US19330.
PR 07-OCT-1998; 98WO-US21141.
PR 01-DEC-1998; 98WO-US25108.
PR 08-MAR-1999; 99WO-US05028.
PR 14-MAY-1999; 99WO-US10733.
PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.
PR 15-SEP-1999; 99WO-US21090.
PR 01-DEC-1999; 99WO-US28301.
PR 02-DEC-1999; 99WO-US28551.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05841.
PR 15-MAR-2000; 2000WO-US06884.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 29-AUG-2001; 2001WO-US27099.
PR 18-SEP-1997; 97US-059263P.
PR 18-SEP-1997; 97US-059266P.
PR 17-OCT-1997; 97US-062250P.
PR 21-OCT-1997; 97US-063486P.
PR 24-OCT-1997; 97US-063120P.
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PR 28-OCT-1997; 97US-063540P.
PR 28-OCT-1997; 97US-063541P.
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PR 24-NOV-1997; 97US-066466P.
PR 24-NOV-1997; 97US-066772P.
PR 11-DEC-1997; 97US-069335P.
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PR 10-MAR-1998; 98US-077450P.
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PR 20-MAR-1998; 98US-078886P.

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PR 08-APR-1998; 98US-081049P.
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PR 09-APR-1998; 98US-081195P.
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PR 21-APR-1998; 98US-082568P.
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PR 22-APR-1998; 98US-082797P.
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PR 05-MAY-1998; 98US-084366P.
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PR 24-JUL-1998; 98US-094006P.
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PR 18-AUG-1998; 98US-096949P.
PR 18-AUG-1998; 98US-096959P.
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PR 26-AUG-1998; 98US-097952P.
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PR 26-AUG-1998; 98US-097955P.
PR 26-AUG-1998; 98US-097971P.
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PR 26-AUG-1998; 98US-098014P.
PR 01-SEP-1998; 98US-098716P.
PR 01-SEP-1998; 98US-098723P.
PR 02-SEP-1998; 98US-098803P.
PR 02-SEP-1998; 98US-098821P.
PR 02-SEP-1998; 98US-098843P.
PR 09-SEP-1998; 98US-099602P.
PR 10-SEP-1998; 98US-099741P.
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PR 10-SEP-1998; 98US-099812P.

Query Match 100.0%; Score 469; DB 24; Length 92;
Best Local Similarity 100.0%; Pred. No. 1.1e-43;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MIHLGHILFLLLLPVAAAQTTPGERSSLPAFYPGTSGSCSGCGSLSLPLLAGLVAADAVA 60
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Db          1 MIHLGHILFLLLLPVAAAQTTPGERSSLPAFYPGTSGSCSGCGSLSLPLLAGLVAADAVA 60

Qy         61 SLLIVGAVFLCARPRRSPAQDGKVYINMPGRG 92
              ||||||||||||||||||||||||||||||||
Db         61 SLLIVGAVFLCARPRRSPAQDGKVYINMPGRG 92
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RESULT 6
ABU71426
ID ABU71426 standard; Protein; 92 AA.
XX
AC ABU71426;
XX
DT 09-JUN-2003 (first entry)
XX
DE Human neoplasia inhibiting PRO polypeptide PRO1157.
XX
KW Human; tumour; cancer; neoplasia; liver cancer; sarcoma;
KW breast cancer; ovarian cancer; renal cancer; colorectal cancer; melanoma;

KW uterine cancer; prostate cancer; lung cancer; bladder cancer; leukaemia;
KW gastric cancer; pancreatic cancer; vulval cancer; thyroid cancer;
KW central nervous system cancer; hepatic carcinoma; glioblastoma;
KW neuronal disorder; glial disorder; astrocytal disorder;
KW hypothalamic disorder; glandular disorder; macrophagal disorder;
KW epithelial disorder; stromal disorder; blastocoelic disorder;
KW inflammatory disorder; angiogenic disorder; immunologic disorder.
XX
OS Homo sapiens.
XX
PN US2002192209-A1.
XX
PD 19-DEC-2002.
XX
PF 30-NOV-2001; 2001US-0001054.
XX
PR 10-SEP-1998; 98WO-US18824.
PR 05-JAN-1999; 99WO-US00106.
PR 08-MAR-1999; 99WO-US05028.
PR 20-APR-1999; 99WO-US08615.
PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.
PR 08-SEP-1999; 99WO-US20594.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US28551.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30999.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 02-MAR-2000; 2000WO-US05841.
PR 15-MAR-2000; 2000WO-US06884.
PR 30-MAR-2000; 2000WO-US08439.
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PR 04-SEP-2001; 2001US-0946374.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W, Kabakoff RC;
PI Shelton DL, Smith V, Watanabe CK, Wood WI;
XX
DR WPI; 2003-328851/31.
DR N-PSDB; ACA57999.
XX
PT Novel isolated PRO polypeptides e.g. PRO240, PRO381, PRO540, useful for
PT treating tumor, preferably cancer, or for treating neuronal, glial,
PT hypothalamic, stromal, inflammatory, angiogenic and immunologic
PT disorders -
XX
PS Claim 32; Fig 20; 186pp; English.
XX
CC The invention relates to an isolated secreted and transmembrane
CC polypeptide, designated as PRO polypeptide, PRO polypeptide lacking its
CC associated signal peptide or PRO polypeptide extracellular domain with or
CC without its associated signal peptide. The PRO polypeptide or an antibody
CC binding to it is useful for inhibiting the growth of a tumor cell. A
CC composition containing a PRO polypeptide is useful for inhibiting
CC neoplastic cell growth or for treating a tumour, preferably cancer (such
CC as liver, breast, ovarian, renal, colorectal, uterine, prostate, lung,
CC bladder, gastric, pancreatic, vulval, thyroid, central nervous system
CC cancer, hepatic carcinomas, sarcomas, glioblastomas, melanoma or
CC leukaemia) in a mammal. The PRO polypeptide is useful for identifying its
CC agonists. The PRO polypeptide or an antibody binding to it is useful in
CC the preparation of a medicament for treating a condition which is
CC responsive to the PRO polypeptide or an antibody binding to it. The PRO
CC polypeptide or an antibody binding to it is also useful for treating
CC neuronal, glial, astrocytal, hypothalamic, glandular, macrophagal,
CC epithelial, stromal, blastocoelic, inflammatory, angiogenic and
CC immunologic disorders. The present sequence represents the amino acid
CC sequence of a PRO polypeptide of the invention.
XX
SQ Sequence 92 AA;

Query Match 100.0%; Score 469; DB 24; Length 92;
Best Local Similarity 100.0%; Pred. No. 1.1e-43;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          61 SLLIVGAVFLCARPRRSPAQDGKVYINMPGRG 92
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RESULT 7
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DT 19-MAY-2003 (first entry)
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XX
KW Human; PRO; secreted protein; transmembrane protein;
KW cytostatic; antiarthritic; osteopathic; adrenal tumour; lung tumour;
KW colon tumour; breast tumour; prostate tumour; rectal tumour;
KW cervical tumour; liver tumour; TNF-alpha release; arthritis;
KW tumour necrosis factor alpha; chondrocyte cell; bone disorder;
KW cartilage disorder; sports injury.
XX
OS Homo sapiens.
XX
PN US2003036156-A1.
XX
PD 20-FEB-2003.
XX
PF 02-JUL-2002; 2002US-0188767.
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Db         61 SLLIVGAVFLCARPRRSPAQDGKVYINMPGRG 92
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RESULT 8
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ID ABU66124 standard; Protein; 92 AA.
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AC ABU66124;
XX
DT 20-MAY-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO1157.
XX
KW Human; secreted protein; transmembrane protein; cytostatic;
KW gene Therapy; TNF-Agonist-Alpha; chondrocyte stimulator; tumour;
KW adrenal tumour; lung tumour; colon tumour; breast tumour;
KW prostate tumour; rectal tumour; cervical tumour; liver tumour.
XX
OS Homo sapiens.
XX
PN US2003036157-A1.
XX
PD 20-FEB-2003.
XX
PF 02-JUL-2002; 2002US-0188769.
XX
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RESULT 9
ABU67628
ID ABU67628 standard; Protein; 92 AA.
XX
AC ABU67628;
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DT 29-MAY-2003 (first entry)
XX
DE Human secreted/transmembrane protein (PRO) #223.
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KW Human; secreted and transmembrane protein; PRO; TNF-alpha;
KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KW tissue typing.
XX
OS Homo sapiens.
XX
PN US2003036162-A1.
XX
PD 20-FEB-2003.
XX
PF 12-JUL-2002; 2002US-0194423.
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PR 16-SEP-1998; 98WO-US19330.
PR 07-OCT-1998; 98WO-US21141.
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PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05841.
PR 15-MAR-2000; 2000WO-US06884.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
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PR 08-NOV-2000; 2000WO-US30952.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 29-AUG-2001; 2001WO-US27099.
PR 26-JUN-1998; 98US-0105413.
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PR 06-AUG-2001; 2001US-0924419.
PR 13-AUG-2001; 2001US-0929404.
PR 16-AUG-2001; 2001US-0931836.
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PR 04-SEP-2001; 2001US-0946374.
PR 15-JAN-2002; 2002US-0052586.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2003-332039/31.
DR N-PSDB; ACA05922.
XX
PT New secreted and transmembrane PRO polypeptides and nucleic acids,
PT useful in gene therapy, in chromosome and gene mapping, as chromosome
PT markers, in tissue typing, and in chromosome identification -
XX
PS Claim 11; Fig 446; 706pp; English.
XX
CC The invention discloses human nucleic acids encoding secreted and
CC transmembrane (PRO) polypeptides. Also disclosed is an antibody that
CC specifically binds to the PRO polypeptide, a method for stimulating the
CC release of tumour necrosis factor alpha (TNF-alpha) from human blood by
CC contacting the blood a PRO polypeptide, a method for stimulating the
CC proliferation or differentiation of chondrocyte cells by contacting the
CC cells with a PRO polypeptide, a method for detecting the presence of a
CC tumour in a mammal and an oligonucleotide probe derived from any of the
CC PRO nucleotide sequences. The nucleotide sequences are useful as probes,
CC in chromosome and gene mapping, in generating antisense RNA and DNA, in
CC preparing PRO polypeptides by recombinant techniques and in gene therapy
CC (e.g. for replacement of defective gene). The PRO polypeptides are useful
CC as molecular weight markers for protein electrophoresis purposes, for
CC chromosome identification, as chromosome markers, as therapeutic agents,
CC for stimulating the release of TNF-alpha from human blood, for
CC stimulating the proliferation or differentiation of chondrocytes and
CC detecting the presence of a tumour. The PRO polypeptides and nucleic
CC acids may also be used diagnostically for tissue typing. The sequences
CC presented in ABU67406-ABU67710 are the PRO polypeptides of the invention.
XX
SQ Sequence 92 AA;

Query Match 100.0%; Score 469; DB 24; Length 92;
Best Local Similarity 100.0%; Pred. No. 1.1e-43;
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Db         61 SLLIVGAVFLCARPRRSPAQDGKVYINMPGRG 92
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RESULT 10
ABG76299
ID ABG76299 standard; Protein; 92 AA.
XX
AC ABG76299;
XX
DT 10-MAY-2003 (first entry)
XX
DE Amino acid sequence for human Zsig16.

XX
KW Human; transmembrane protein; Zsig16; peripheral blood lymphocyte;
KW lymphocyte marker; lymphocyte cell type; cancerous cell.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..18
FT /label= Signal_peptide
FT /note= "Specifically claimed in Claim 4"
FT Protein 19..92
FT /label= Mature_Zsig16
FT Domain 19..47
FT /label= Extracellular_domain
FT /note= "Specifically claimed in Claim 1"
FT Domain 48..70
FT /label= Transmembrane_domain
FT /note= "Specifically claimed in Claim 2"
FT Domain 71..92
FT /label= Intracellular_domain
FT /note= "Specifically claimed in Claim 3"
XX
PN US2002164764-A1.
XX
PD 07-NOV-2002.
XX
PF 18-OCT-2001; 2001US-0982405.
XX
PR 17-SEP-1998; 98US-100865P.
PR 13-SEP-1999; 99US-0394767.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Sheppard PO, Haldeman BA, Holly RD;
XX
DR WPI; 2003-298699/29.
DR N-PSDB; ABX11764.
XX
PT New Zsig16 polypeptides, useful in immunological diagnostic assays for
PT Zsig16 gene expression -
XX
PS Claim 5; Page 3; 30pp; English.
XX
CC The present invention relates to the isolation of a novel human
CC transmembrane protein designated Zsig16, and the polynucleotide
CC sequence encoding it. Zsig16 is expressed by human peripheral blood
CC lymphocytes. It may be used as a lymphocyte "marker" to distinguish
CC between normal lymphocyte cell types as well as between normal and
CC cancerous cells. The Zsig16 polypeptide is useful in diagnosis,
CC prognosis, and therapy. The present sequence represents human Zsig16.
XX
SQ Sequence 92 AA;

Query Match 100.0%; Score 469; DB 24; Length 92;
Best Local Similarity 100.0%; Pred. No. 1.1e-43;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 SLLIVGAVFLCARPRRSPAQDGKVYINMPGRG 92
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Db         61 SLLIVGAVFLCARPRRSPAQDGKVYINMPGRG 92
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RESULT 11
ABU65486
ID ABU65486 standard; Protein; 92 AA.
XX
AC ABU65486;
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DT 16-MAY-2003 (first entry)

XX
DE Human PRO polypeptide #223.
XX
KW Human; PRO; cytostatic; chromosome mapping; gene mapping;
KW protein electrophoresis; tumour necrosis factor-alpha; TNF-alpha; blood;
KW chondrocyte differentiation; chondrocyte proliferation; tumour.
XX
OS Homo sapiens.
XX
PN US2003032102-A1.
XX
PD 13-FEB-2003.
XX
PF 17-JUN-2002; 2002US-0173697.
XX
PR 16-SEP-1998; 98WO-US19330.
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PR 14-MAY-1999; 99WO-US10733.
PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.
PR 15-SEP-1999; 99WO-US21090.
PR 01-DEC-1999; 99WO-US28301.
PR 02-DEC-1999; 99WO-US28551.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
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PR 02-MAR-2000; 2000WO-US05841.
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PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
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PR 30-MAY-2000; 2000WO-US14941.
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PR 10-AUG-1998; 98US-096012P.
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Query Match 100.0%; Score 469; DB 24; Length 92;
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Db         61 SLLIVGAVFLCARPRRSPAQDGKVYINMPGRG 92
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RESULT 12
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AC ABU58622;
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DT 15-APR-2003 (first entry)
XX
DE Human PRO polypeptide #223.
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KW Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach;
KW liver; dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;
KW antibody-dependent enzyme mediated prodrug therapy.
XX
OS Homo sapiens.
XX
PN US2003027272-A1.
XX
PD 06-FEB-2003.
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PF 21-JUN-2002; 2002US-0176492.
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DT 26-MAR-2003 (first entry)
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KW antiarthritic; vulnerary; tumour necrosis factor-alpha;
KW chondrocyte cell proliferation; chondrocyte cell differentiation;
KW tumour; adrenal tumour; lung tumour; colon tumour; breast tumour;
KW prostate tumour; rectal tumour; cervical tumour; liver tumour;
KW bone disorder; cartilage disorder; arthritis; sports injury.
XX
OS Homo sapiens.
XX
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AC ABU57153;
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DT 04-APR-2003 (first entry)
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KW Human; PRO; tumour necrosis factor-alpha; blood; cancer;
KW chondrocyte cell; tumour; adrenal tumour; lung; colon; breast; prostate;
KW kidney; rectum; cervix; liver; bone disorder; cartilage disorder;
KW arthritis; sports injury; genetic disorder; antiarthritic; vulnerary.
XX
OS Homo sapiens.

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PR 16-JUN-1998; 98US-089512P.
PR 16-JUN-1998; 98US-089514P.
PR 17-JUN-1998; 98US-089538P.
PR 17-JUN-1998; 98US-089598P.
PR 17-JUN-1998; 98US-089653P.
PR 18-JUN-1998; 98US-089908P.
PR 19-JUN-1998; 98US-089952P.
PR 22-JUN-1998; 98US-090246P.
PR 22-JUN-1998; 98US-090252P.
PR 22-JUN-1998; 98US-090254P.
PR 24-JUN-1998; 98US-090429P.
PR 24-JUN-1998; 98US-090435P.
PR 24-JUN-1998; 98US-090444P.
PR 24-JUN-1998; 98US-090461P.
PR 24-JUN-1998; 98US-090535P.
PR 24-JUN-1998; 98US-090540P.
PR 25-JUN-1998; 98US-090676P.
PR 25-JUN-1998; 98US-090678P.
PR 25-JUN-1998; 98US-090688P.
PR 25-JUN-1998; 98US-090690P.

PR 25-JUN-1998; 98US-090694P.
PR 25-JUN-1998; 98US-090695P.
PR 25-JUN-1998; 98US-090696P.
PR 26-JUN-1998; 98US-090862P.
PR 26-JUN-1998; 98US-090863P.
PR 26-JUN-1998; 98US-091010P.
PR 01-JUL-1998; 98US-091359P.
PR 01-JUL-1998; 98US-091544P.
PR 02-JUL-1998; 98US-091478P.
PR 02-JUL-1998; 98US-091486P.
PR 02-JUL-1998; 98US-091626P.
PR 02-JUL-1998; 98US-091628P.
PR 02-JUL-1998; 98US-091632P.
PR 24-JUL-1998; 98US-094006P.
PR 04-AUG-1998; 98US-095282P.
PR 10-AUG-1998; 98US-095998P.
PR 10-AUG-1998; 98US-096012P.
PR 17-AUG-1998; 98US-096757P.
PR 17-AUG-1998; 98US-096766P.
PR 17-AUG-1998; 98US-096867P.
PR 17-AUG-1998; 98US-096891P.
PR 17-AUG-1998; 98US-096897P.
PR 18-AUG-1998; 98US-096949P.
PR 18-AUG-1998; 98US-096959P.
PR 18-AUG-1998; 98US-097022P.
PR 26-AUG-1998; 98US-097952P.
PR 26-AUG-1998; 98US-097954P.
PR 26-AUG-1998; 98US-097955P.
PR 26-AUG-1998; 98US-097971P.
PR 26-AUG-1998; 98US-097974P.
PR 26-AUG-1998; 98US-098014P.
PR 01-SEP-1998; 98US-098716P.
PR 01-SEP-1998; 98US-098723P.
PR 02-SEP-1998; 98US-098803P.
PR 02-SEP-1998; 98US-098821P.
PR 02-SEP-1998; 98US-098843P.
PR 09-SEP-1998; 98US-099602P.
PR 10-SEP-1998; 98US-099741P.
PR 10-SEP-1998; 98US-099754P.
PR 10-SEP-1998; 98US-099763P.

Query Match 100.0%; Score 469; DB 24; Length 92;
Best Local Similarity 100.0%; Pred. No. 1.1e-43;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MIHLGHILFLLLLPVAAAQTTPGERSSLPAFYPGTSGSCSGCGSLSLPLLAGLVAADAVA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MIHLGHILFLLLLPVAAAQTTPGERSSLPAFYPGTSGSCSGCGSLSLPLLAGLVAADAVA 60

Qy         61 SLLIVGAVFLCARPRRSPAQDGKVYINMPGRG 92
              ||||||||||||||||||||||||||||||||
Db         61 SLLIVGAVFLCARPRRSPAQDGKVYINMPGRG 92
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RESULT 15
ABU10732
ID ABU10732 standard; Protein; 92 AA.
XX
AC ABU10732;
XX
DT 03-FEB-2003 (first entry)
XX
DE Human secreted/transmembrane protein #223.
XX
KW Human; secreted and transmembrane protein; blood;
KW tumour necrosis factor-alpha; chondrocyte cell proliferation;
KW chondrocyte cell differentiation; tumour; adrenal tumour; lung tumour;
KW colon tumour; breast tumour; prostate tumour; rectal tumour;
KW cervical tumour; liver tumour; bone disorder; cartilage disorder;
KW arthritis; sports injury.
XX
OS Homo sapiens.
XX

PN US2002127584-A1.
XX
PD 12-SEP-2002.
XX
PF 15-JAN-2002; 2002US-0052586.
XX
PR 16-SEP-1998; 98WO-US19330.
PR 07-OCT-1998; 98WO-US21141.
PR 01-DEC-1998; 98WO-US25108.
PR 06-JAN-1999; 2000WO-US00219.
PR 08-MAR-1999; 99WO-US05028.
PR 14-MAY-1999; 99WO-US10733.
PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.
PR 15-SEP-1999; 99WO-US21090.
PR 01-DEC-1999; 99WO-US28301.
PR 02-DEC-1999; 99WO-US28551.
PR 30-DEC-1999; 99WO-US31274.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05841.
PR 15-MAR-2000; 2000WO-US06884.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 29-AUG-2001; 2001WO-US27099.
PR 18-SEP-1997; 97US-059263P.
PR 18-SEP-1997; 97US-059266P.
PR 17-OCT-1997; 97US-062250P.
PR 21-OCT-1997; 97US-063486P.
PR 24-OCT-1997; 97US-063120P.
PR 24-OCT-1997; 97US-063121P.
PR 28-OCT-1997; 97US-063540P.
PR 28-OCT-1997; 97US-063541P.
PR 28-OCT-1997; 97US-063544P.
PR 28-OCT-1997; 97US-063564P.
PR 29-OCT-1997; 97US-063734P.
PR 31-OCT-1997; 97US-063870P.
PR 31-OCT-1997; 97US-064103P.
PR 13-NOV-1997; 97US-065311P.
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PR 11-DEC-1997; 97US-069335P.
PR 12-DEC-1997; 97US-069425P.
PR 17-DEC-1997; 97US-069870P.
PR 18-DEC-1997; 97US-068017P.
PR 10-MAR-1998; 98US-077450P.
PR 11-MAR-1998; 98US-077632P.
PR 11-MAR-1998; 98US-077649P.
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PR 27-MAR-1998; 98US-079664P.
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PR 31-MAR-1998; 98US-080107P.
PR 31-MAR-1998; 98US-080194P.
PR 01-APR-1998; 98US-080327P.
PR 01-APR-1998; 98US-080333P.

PR 08-APR-1998; 98US-081049P.
PR 08-APR-1998; 98US-081070P.
PR 09-APR-1998; 98US-081195P.
PR 15-APR-1998; 98US-081838P.
PR 21-APR-1998; 98US-082568P.
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PR 22-APR-1998; 98US-082797P.
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PR 29-APR-1998; 98US-083495P.
PR 29-APR-1998; 98US-083496P.
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PR 29-APR-1998; 98US-083559P.
PR 05-MAY-1998; 98US-084366P.
PR 06-MAY-1998; 98US-084414P.
PR 07-MAY-1998; 98US-084639P.
PR 07-MAY-1998; 98US-084640P.
PR 07-MAY-1998; 98US-084643P.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2003-066893/06.
DR N-PSDB; ABX16808.
XX
PT Novel isolated PRO polypeptides e.g., PRO1079, PRO827, PRO791, PRO1131,
PT PRO1316, PRO1183, PRO1343, PRO1760, PRO1567 or PRO4333, useful for
PT stimulating release of tumor necrosis factor-alpha from human blood -
XX
PS Claim 11; Fig 446; 701pp; English.
XX
CC The invention relates to an isolated PRO polypeptide comprising at least
CC 80% sequence identity to the protein sequences appearing as ABU10510-
CC ABU10814 (including a version lacking its associated signal peptide, or
CC an isolated extracellular domain of a PRO polypeptide with or without
CC its associated signal peptide. Also included are the nucleic acids
CC encoding the PRO proteins (being secreted and transmembrane proteins)
CC appearing as ABX16586-ABX16590, PRO expression vectors, host cells,
CC chimaeric PRO fusion proteins, an anti-PRO antibody and a PRO
CC derived oligonucleotide sequence. The PRO polypeptides are useful for
CC stimulating release of tumour necrosis factor-alpha from human blood.
CC The PRO polypeptide PRO6029 is useful for stimulating proliferation or
CC differentiation of chondrocyte cells. The PRO polypeptides as specified
CC in the specification and having differential expression in tumour cells,
CC are useful for detecting presence of tumour in a mammal (such as adrenal
CC tumour, lung tumour, colon tumour, breast tumour, prostate tumour, rectal
CC tumour, cervical tumour or liver tumour. The PRO polypeptide PRO6029 is
CC useful for treating various bone and/or cartilage disorders such as
CC arthritis, and sports injuries. The PRO polypeptides are useful for
CC screening compounds to identify ant/agonists. PRO nucleic acids
CC are useful as hybridisation probes, in chromosome and gene mapping,
CC in the generation of anti-sense RNA and DNA, for the preparation of PRO
CC polypeptides and for generating knock-out animals. The present
CC sequence represents a PRO polypeptide.
XX
SQ Sequence 92 AA;

Query Match 100.0%; Score 469; DB 24; Length 92;
Best Local Similarity 100.0%; Pred. No. 1.1e-43;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MIHLGHILFLLLLPVAAAQTTPGERSSLPAFYPGTSGSCSGCGSLSLPLLAGLVAADAVA 60

Qy         61 SLLIVGAVFLCARPRRSPAQDGKVYINMPGRG 92
              ||||||||||||||||||||||||||||||||
Db         61 SLLIVGAVFLCARPRRSPAQDGKVYINMPGRG 92
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Search completed: January 29, 2004, 08:47:54

Job time : 43 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 29, 2004, 08:46:18 ; Search time 21 Seconds
(without alignments)
421.310 Million cell updates/sec

Title: US-09-982-405-2
Perfect score: 469
Sequence: 1 MIHLGHILFLLLLPVAAAQT.....RPRRSPAQDGKVYINMPGRG 92

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	458.5	97.8	131	2	T08788	hypothetical prote
2	77.5	16.5	597	2	B69251	probable electron
3	77	16.4	278	2	C75275	hypothetical prote
4	72.5	15.5	1062	2	T46444	hypothetical prote
5	72	15.4	390	2	I51419	transcription fact
6	72	15.4	548	1	I37577	islet cell antigen
7	71	15.1	396	2	G69808	multidrug resistan
8	70.5	15.0	190	2	H83034	hypothetical prote
9	70	14.9	450	2	F95360	probable transmemb
10	68.5	14.6	147	2	A43547	T-cell surface gly
11	68.5	14.6	342	2	D88924	protein R02C2.5 [i
12	68	14.5	93	2	C90192	conserved hypothet
13	68	14.5	175	2	A39171	T-cell surface gly
14	67.5	14.4	277	1	S68421	endopeptidase Clp
15	67	14.3	142	2	S58082	transmembrane prot
16	67	14.3	401	2	C83109	probable transport
17	66.5	14.2	208	2	A82712	endopeptidase Clp
18	66.5	14.2	287	2	A72751	hypothetical prote
19	66	14.1	158	2	T46410	hypothetical prote
20	66	14.1	184	2	B84259	hypothetical prote
21	66	14.1	427	2	E72488	probable tryptopha
22	66	14.1	577	1	VGBEGI	glycoprotein E - s
23	65.5	14.0	140	2	A57544	BM88 antigen - pig
24	65.5	14.0	193	1	D64088	endopeptidase Clp
25	65.5	14.0	267	2	T46087	hypothetical prote
26	65.5	14.0	343	2	T42549	cell fusion protei
27	65	13.9	163	2	G75435	hypothetical prote
28	65	13.9	228	2	F70934	probable lpqN prot
29	65	13.9	269	2	H75576	cobalamin synthase
30	65	13.9	326	2	A46676	CD68 homolog macro
31	65	13.9	376	2	S57867	oncogene 1 - human
32	65	13.9	395	2	E90896	probable transport
33	65	13.9	395	2	B85721	probable transport
34	65	13.9	436	2	JN0591	serotonin receptor
35	65	13.9	437	2	I57942	5-hydroxytryptamin
36	65	13.9	658	2	T03416	traG protein - Agr
37	65	13.9	658	2	AB3243	conjugal transfer
38	65	13.9	786	2	S22155	oncogene 1 (tre-2
39	65	13.9	827	2	A95877	hypothetical prote
40	64.5	13.8	207	1	B36575	endopeptidase Clp
41	64.5	13.8	207	2	C90690	endopeptidase Clp
42	64.5	13.8	207	2	G85540	endopeptidase Clp
43	64.5	13.8	207	2	AC0558	ATP-dependent clp
44	64.5	13.8	294	2	B70975	hypothetical prote
45	64.5	13.8	387	2	A45827	pigment production

ALIGNMENTS

RESULT 1
T08788
hypothetical protein DKFZp586C1522.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 13-Aug-1999
C;Accession: T08788
R;Koehrer, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, March 1999
A;Reference number: Z16473
A;Accession: T08788
A;Molecule type: mRNA
A;Residues: 1-131 <KOE>
A;Cross-references: EMBL:AL050163
A;Experimental source: adult uterus; clone DKFZp586C1522
C;Genetics:
A;Note: DKFZp586C1522.1

Query Match 97.8%; Score 458.5; DB 2; Length 131;
Best Local Similarity 98.9%; Pred. No. 4.2e-38;
Matches 92; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Db         39 MIHLGHILFLLLLPVAAAQTTPGERSSLPAFYPGTSGSCSGCGSLSLPLLAGLVAADAVA 98

Qy         61 SLLIVGAVFLCARPRRSPAQ-DGKVYINMPGRG 92
              |||||||||||||||||||| ||||||||||||
Db         99 SLLIVGAVFLCARPRRSPAQEDGKVYINMPGRG 131
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RESULT 2
B69251
probable electron transfer protein AF0010 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C;Accession: B69251
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: B69251
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-597 <KLE>
A;Cross-references: GB:AE001106; GB:AE000782; NID:g2689429; PIDN:AAB91224.1; PID:g265064
C;Superfamily: ferredoxin [2Fe-2S] homology
C;Keywords: 2Fe-2S; iron-sulfur protein; metalloprotein
F;20-80/Domain: ferredoxin [2Fe-2S] homology <FER>

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F;35,41,44,79/Binding site: 2Fe-2S cluster (Cys) (covalent) #status predicted

  Query Match             16.5%;  Score 77.5;  DB 2;  Length 597;
  Best Local Similarity   41.5%;  Pred. No. 4.8;
  Matches   27;  Conservative    7;  Mismatches   26;  Indels    5;  Gaps    3;

Qy          6 HILFLLLLP--VAAAQTTPGERS--SLPAFYPGTSGSCSGCGSLSLPLLAGLVAADAVAS 61
              | ||  : |  :  :  ||  |   | ||   |   :  |  | ||||:|| | |||||:
Db        285 HHLFFGIEPRFIGVSPFTPAVRRGVSFPAEDVGLRINRKGYVS-SLPLVAGFVGADAVAN 343

Qy         62 LLIVG 66
              : | |
Db        344 IAITG 348


RESULT 3
C75275
hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C;Accession: C75275
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: C75275
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-278 <WHI>
A;Cross-references: GB:AE002073; GB:AE000513; NID:g6460244; PIDN:AAF11982.1; PID:g646025
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR2437
A;Map position: 1

  Query Match             16.4%;  Score 77;  DB 2;  Length 278;
  Best Local Similarity   28.8%;  Pred. No. 2.7;
  Matches   30;  Conservative   18;  Mismatches   26;  Indels   30;  Gaps    6;

Qy          1 MIHLGHIL---FLLLLPVAAAQTTPGERS-------------SLPAFYP----GTSGSCS 40
              :: | | |     |:|| |    |  ||: :             :: |||     |  |: |
Db         36 VVALSHTLSAVALVLLAVGLGQPMPGQTALLWGAGAGLLGMGAVVAFYRALALGPMGAVS 95

Qy         41 -GCGSLS--LPLLAGLVAADAVASL-------LIVGAVFLCARP 74
               | |:||  :|: |||:| :::  |       :::|   |  ||
Db         96 VGAGALSAVVPVGAGLLAGESLGRLGSLGALGVLLGTALLSFRP 139


RESULT 4
T46444
hypothetical protein DKFZp434N1427.1 - human
C;Species: Homo sapiens (man)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
C;Accession: T46444
R;Bloecker, H.; Boecher, M.; Brandt, P.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, January 2000
A;Reference number: Z23032
A;Accession: T46444
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1062 <AAA>
A;Cross-references: EMBL:AL137701
A;Experimental source: adult testis; clone DKFZp434N1427
C;Genetics:
A;Note: DKFZp434N1427.1

  Query Match             15.5%;  Score 72.5;  DB 2;  Length 1062;
  Best Local Similarity   35.6%;  Pred. No. 24;
  Matches   31;  Conservative    9;  Mismatches   28;  Indels   19;  Gaps    3;

Qy          7 ILFLLLLPVAAAQTTPGERSSLPAFYPGTSGSCSG----CGSLSLP-----LLAGLVAAD 57
                :| |||||: |||    | :::| |    |  |  :     | :| ||      |||    |
Db        795 LLLLLLLPLLAAQGGGGLQAALLALEVGLVGLGASYLLLCTALHLPSSLFLLLAQGTALG 854

Qy         58 AVASL----------LIVGAVFLCARP 74
              ||  |          | :|| :| | |
Db        855 AVLGLSWRRGLMGVPLGLGAAWLLAWP 881


RESULT 5
I51419
transcription factor xGATA-4a - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 08-Dec-2000
C;Accession: I51419
R;Kelley, C.; Blumberg, H.; Zon, L.I.; Evans, T.
Development 118, 817-827, 1993
A;Title: GATA-4 is a novel transcription factor expressed in endocardium of the developi
A;Reference number: I51419; MUID:94357077; PMID:8076520
A;Accession: I51419
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-390 <KEL>
A;Cross-references: GB:L13701; NID:g311049; PIDN:AAA63686.1; PID:g311050
C;Superfamily: transcription factor GATA-4; GATA-type zinc finger homology
C;Keywords: zinc finger
F;180-233/Domain: GATA-type zinc finger homology <GZF1>
F;234-287/Domain: GATA-type zinc finger homology <GZF2>

  Query Match             15.4%;  Score 72;  DB 2;  Length 390;
  Best Local Similarity   36.2%;  Pred. No. 11;
  Matches   17;  Conservative    6;  Mismatches   22;  Indels    2;  Gaps    1;

Qy          5 GHILFLLLLPVAAAQTTPGERSSLPAF--YPGTSGSCSGCGSLSLPL 49
              ||    :|  :   |:  | ||||     :||    |  ||::| ||
Db        147 GHFEGSMLHSLQGRQSLSGRRSSLEFLEEFPGEGRECVNCGAMSTPL 193


RESULT 6
I37577
islet cell antigen 512 - human
N;Alternate names: islet cell autoantigen 3
N;Contains: protein-tyrosine-phosphatase (EC 3.1.3.48)
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: I37577; S18121
R;Rabin, D.U.; Pleasic, S.M.; Shapiro, J.A.; Yoo-Warren, H.; Oles, J.; Hicks, J.M.; Gold
J. Immunol. 152, 3183-3188, 1994
A;Title: Islet cell antigen 512 is a diabetes-specific islet autoantigen related to prot
A;Reference number: I37577; MUID:94194080; PMID:8144912
A;Accession: I37577
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-548 <RES>
A;Cross-references: EMBL:X62899; NID:g32612; PIDN:CAA44688.1; PID:g32613
C;Genetics:
A;Gene: GDB:ICA3
A;Cross-references: GDB:385512
C;Superfamily: protein-tyrosine-phosphatase, receptor type N; protein-tyrosine-phosphata
C;Keywords: phosphoprotein; phosphoric monoester hydrolase; transmembrane protein; tyros
F;196-212/Domain: transmembrane #status predicted <TMN>
F;346-548/Domain: protein-tyrosine-phosphatase homology #status atypical <PTP>
F;521/Active site: Cys (phosphocysteine intermediate) #status predicted

  Query Match             15.4%;  Score 72;  DB 1;  Length 548;
  Best Local Similarity   41.8%;  Pred. No. 15;
  Matches   23;  Conservative    4;  Mismatches   24;  Indels    4;  Gaps    1;

Qy         19 QTTPGERSSLPAFYPGTSGSCSGCGSLSLPLLAGLVAADAVASLLIVGAVFLCAR 73
              ||  |:|    |  | |: | |   |    :|  |||   || ||:  || || |
Db        163 QTGVGQREEAAAVLPQTAHSTSPMRS----VLLTLVALAGVAGLLVALAVALCVR 213


RESULT 7
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 29, 2004, 08:42:52 ; Search time 11 Seconds
(without alignments)
393.314 Million cell updates/sec

Title: US-09-982-405-2
Perfect score: 469
Sequence: 1 MIHLGHILFLLLLPVAAAQT.....RPRRSPAQDGKVYINMPGRG 92

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	80.5	17.2	354	1	RNFD_PSEST	Q9evn4 pseudomonas
2	75	16.0	2214	1	SORL_HUMAN	Q92673 h sortilin-
3	74.5	15.9	180	1	PTTG_HUMAN	P53801 homo sapien
4	74	15.8	426	1	BRNQ_CORGL	O06754 corynebacte
5	73.5	15.7	113	1	TYBP_HUMAN	O43914 homo sapien
6	72	15.4	390	1	GA5A_XENLA	P43695 xenopus lae
7	72	15.4	979	1	PTPN_HUMAN	Q16849 homo sapien
8	70.5	15.0	198	1	CLPP_THETN	Q8rc25 thermoanaer
9	70	14.9	114	1	TYBP_MOUSE	O54885 mus musculu
10	68.5	14.6	147	1	CD3G_SHEEP	P18439 ovis aries
11	68	14.5	485	1	C6U1_DROME	Q9v979 drosophila
12	67.5	14.4	277	1	CLPP_HUMAN	Q16740 homo sapien
13	67	14.3	142	1	TM10_PIG	Q29102 sus scrofa
14	67	14.3	404	1	GAT5_MOUSE	P97489 mus musculu
15	67	14.3	979	1	PTPN_BOVIN	P56722 bos taurus
16	66.5	14.2	208	1	CLPP_XYLFA	Q9pe41 xylella fas
17	66.5	14.2	210	1	CLPP_AZOBR	Q9x6w8 azospirillu
18	66.5	14.2	272	1	CLPP_MOUSE	O88696 mus musculu
19	66	14.1	427	1	TRB1_AERPE	Q9y8t5 aeropyrum p
20	66	14.1	577	1	VGLE_PRVRI	P08354 pseudorabie
21	66	14.1	828	1	LGR6_HUMAN	Q9hbx8 homo sapien
22	66	14.1	1115	1	E2K3_HUMAN	Q9nzj5 homo sapien
23	65.5	14.0	140	1	BM88_PIG	Q29026 sus scrofa
24	65.5	14.0	193	1	CLPP_HAEIN	P43867 haemophilus
25	65.5	14.0	194	1	CLPP_CLOPE	Q8xkk1 clostridium
26	65.5	14.0	447	1	AMBN_HUMAN	Q9np70 homo sapien
27	65	13.9	247	1	APM1_MOUSE	Q60994 mus musculu
28	65	13.9	326	1	CD68_MOUSE	P31996 mus musculu
29	65	13.9	436	1	5H6_RAT	P31388 rattus norv
30	65	13.9	658	1	TRAG_AGRT5	Q44346 agrobacteri
31	64.5	13.8	184	1	T13C_HUMAN	Q96rj3 homo sapien
32	64.5	13.8	204	1	YX95_MYCTU	Q50730 mycobacteri
33	64.5	13.8	207	1	CLPP_ECOLI	P19245 escherichia
34	64.5	13.8	207	1	CLPP_SALTY	Q91c07 salmonella
35	64.5	13.8	387	1	PIGM_RHOSO	P26698 rhodococcus
36	64.5	13.8	410	1	BHB3_MOUSE	Q99pv5 mus musculu
37	64	13.6	171	1	CD3D_MACFA	Q95li8 macaca fasc
38	64	13.6	393	1	TCR7_VIBAN	P51563 vibrio angu
39	64	13.6	688	1	EOMD_MOUSE	O54839 mus musculu
40	63.5	13.5	173	1	CD3D_RAT	P19377 rattus norv
41	63.5	13.5	193	1	CLPP_PASMU	Q9cjm2 pasteurella
42	63.5	13.5	203	1	CLP1_TREPA	O83520 treponema p
43	63.5	13.5	410	1	BHB3_RAT	O35779 rattus norv
44	63.5	13.5	448	1	EDAR_HUMAN	Q9une0 homo sapien
45	63	13.4	243	1	ZIPA_XANAC	Q8pm10 xanthomonas

ALIGNMENTS

RESULT 1
RNFD_PSEST
ID RNFD_PSEST STANDARD; PRT; 354 AA.
AC Q9EVN4;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Electron transport complex protein rnfD (Nitrogen fixation protein
DE rnfD).
GN RNFD.
OS Pseudomonas stutzeri (Pseudomonas perfectomarina).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=316;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A15;
RA Desnoues N., Lin M., Elmerich C.;
RT "Organisation of nif genes in Pseudomonas stutzeri A15, a rice
RT endophyte.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: Required for nitrogen fixation. May be part of a
CC membrane complex functioning as an intermediate in the electron
CC transport to nitrogenase (By similarity).
CC -!- SUBUNIT: Composed of at least six subunits; rnfA, rnfB, rnfC,
CC rnfD, rnfE and rnfG (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (Potential).
CC -!- SIMILARITY: BELONGS TO THE NQRB/RNFD FAMILY.
CC --

CC --
DR EMBL; AJ297529; CAC03727.1; -.
DR HAMAP; MF_00462; -; 1.
DR InterPro; IPR004338; NQR2_RnfD_RnfE.
DR Pfam; PF03116; NQR2_RnfD_RnfE; 1.
KW Nitrogen fixation; Electron transport; Transmembrane; Inner membrane.
FT TRANSMEM 9 28 POTENTIAL.
FT TRANSMEM 32 54 POTENTIAL.
FT TRANSMEM 61 78 POTENTIAL.
FT TRANSMEM 83 105 POTENTIAL.
FT TRANSMEM 117 137 POTENTIAL.
FT TRANSMEM 200 220 POTENTIAL.
FT TRANSMEM 222 242 POTENTIAL.
FT TRANSMEM 249 269 POTENTIAL.
FT TRANSMEM 277 297 POTENTIAL.
FT TRANSMEM 301 321 POTENTIAL.
SQ SEQUENCE 354 AA; 37563 MW; BB540BDEEA0775B7 CRC64;

Query Match 17.2%; Score 80.5; DB 1; Length 354;

```
  Best Local Similarity   28.8%;  Pred. No. 0.65;
  Matches   36;  Conservative   11;  Mismatches   33;  Indels   45;  Gaps    4;

Qy          4 LGHILFLLLLPVAAAQTTPGERSSLPAFYPGTSGSCSGCGSLSLPLLAG---------- 52
              |||:   | |  :|||   |  : ||||  | ||   |  |  | || |
Db        167 LGHLQTELTLGHSAAQILDGHFALLPAFL-GYSGGSLGETSELLILLGGLWLLALRIIHW 225

Qy         53 ------LVAADAVASL-------------------LIVGAVFLCARPRRSPAQDGKVYI 86
                    |:   |:|:|                   |::||:|:   |  ||      |
Db        226 EIPLGMLLTVGALAALANQIDPQVHGGGLFHLTSGGLLLGALFIATDPVTSP-------I 278

Qy         87 NMPGR 91
              :  ||
Db        279 SRSGR 283


RESULT 2
SORL_HUMAN
ID   SORL_HUMAN     STANDARD;      PRT;  2214 AA.
AC   Q92673; Q92856;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Sortilin-related receptor precursor (Sorting protein-related receptor
DE   containing LDLR class A repeats) (SorLA) (SorLA-1) (Low-density
DE   lipoprotein receptor relative with 11 ligand-binding repeats) (LDLR
DE   relative with 11 ligand-binding repeats) (LR11).
GN   SORL1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=97301565; PubMed=9157966;
RA   Morwald S., Yamazaki H., Bujo H., Kusunoki J., Kanaki T., Seimiya K.,
RA   Morisaki N., Nimpf J., Schneider W.J., Saito Y.;
RT   "A novel mosaic protein containing LDL receptor elements is highly
RT   conserved in humans and chickens.";
RL   Arterioscler. Thromb. Vasc. Biol. 17:996-1002(1997).
RN   [2]
RP   SEQUENCE FROM N.A., SEQUENCE OF N-TERMINUS, AND PARTIAL SEQUENCE.
RC   TISSUE=Brain, and T-cell;
RX   MEDLINE=97094912; PubMed=8940146;
RA   Jacobsen L., Madsen P., Moestrup S.K., Lund A.H., Tommerup N.,
RA   Nykjaer A., Sottrup-Jensen L., Gliemann J., Petersen C.M.;
RT   "Molecular characterization of a novel human hybrid-type receptor that
RT   binds the alpha2-macroglobulin receptor-associated protein.";
RL   J. Biol. Chem. 271:31379-31383(1996).
CC   -!- FUNCTION: LIKELY TO BE A MULTIFUNCTIONAL ENDOCYTIC RECEPTOR, THAT
CC       MAY BE IMPLICATED IN THE UPTAKE OF LIPOPROTEINS AND OF PROTEASES.
CC       BINDS LDL, THE MAJOR CHOLESTEROL-CARRYING LIPOPROTEIN OF PLASMA,
CC       AND TRANSPORTS IT INTO CELLS BY ENDOCYTOSIS. BINDS THE RECEPTOR-
CC       ASSOCIATED PROTEIN (RAP). COULD PLAY A ROLE IN CELL-CELL
CC       INTERACTION.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC   -!- TISSUE SPECIFICITY: EXPRESSED MAINLY IN BRAIN, WHERE IT IS MOST
CC       ABUNDANT IN THE CEREBELLUM, CEREBRAL CORTEX AND THE OCCIPITAL
CC       POLE; LOW EXPRESSION IN THE PUTAMEN AND THE THALAMUS. ACCORDING TO
CC       REF.1, FOUND IN SPINAL CORD, TESTIS, LIVER, KIDNEY AND PANCREAS
CC       WITH DETECTABLE LEVELS IN PLACENTA, LUNG AND HEART. ACCORDING TO
CC       REF.2, EXPRESSED IN THE PROSTATE, OVARY, THYROID AND SPLEEN, BUT
CC       NOT FOUND IN KIDNEY, LIVER, LUNG, SKELETAL MUSCLE, BONE MARROW AND
CC       ADRENALS.
CC   -!- PTM: THE PROPEPTIDE REMOVED IN THE N-TERMINUS MAY BE CLEAVED BY
CC       FURIN OR HOMOLOGOUS PROTEASES.
CC   -!- SIMILARITY: Contains 5 BNR repeats.
CC   -!- SIMILARITY: Contains 1 EGF-like domain.
CC   -!- SIMILARITY: Contains 11 LDL-receptor class A domains.
CC   -!- SIMILARITY: Contains 6 fibronectin type III domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Y08110; CAA69325.1; -.
DR   EMBL; U60975; AAC50891.2; -.
DR   HSSP; P01130; 1AJJ.
DR   Genew; HGNC:11185; SORL1.
DR   MIM; 602005; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0015029; F:internalization receptor activity; TAS.
DR   GO; GO:0004888; F:transmembrane receptor activity; TAS.
DR   GO; GO:0006898; P:receptor mediated endocytosis; TAS.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR002860; GH_BNR.
DR   InterPro; IPR006210; IEGF.
DR   InterPro; IPR002172; LDL_receptor_A.
DR   InterPro; IPR000033; Ldl_receptor_rep.
DR   InterPro; IPR006581; VPS10.
DR   Pfam; PF02012; BNR; 5.
DR   Pfam; PF00041; fn3; 5.
DR   Pfam; PF00057; ldl_recept_a; 11.
DR   Pfam; PF00058; ldl_recept_b; 4.
DR   PRINTS; PR00261; LDLRECEPTOR.
DR   SMART; SM00181; EGF; 1.
DR   SMART; SM00060; FN3; 6.
DR   SMART; SM00192; LDLa; 11.
DR   SMART; SM00135; LY; 5.
DR   SMART; SM00602; VPS10; 1.
DR   PROSITE; PS01186; EGF_2; 1.
DR   PROSITE; PS01209; LDLRA_1; 10.
DR   PROSITE; PS50068; LDLRA_2; 11.
KW   Endocytosis; Receptor; Transmembrane; EGF-like domain; Repeat;
KW   Glycoprotein; LDL; Lipid transport; Cholesterol metabolism; Signal.
FT   SIGNAL       1     28       POTENTIAL.
FT   PROPEP      29     81       REMOVED IN MATURE PROTEIN.
FT   CHAIN       82   2214       SORTILIN-RELATED RECEPTOR.
FT   DOMAIN      82   2137       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM  2138   2158       POTENTIAL.
FT   DOMAIN    2159   2214       CYTOPLASMIC (POTENTIAL).
FT   REPEAT     136    147       BNR 1.
FT   REPEAT     232    243       BNR 2.
FT   REPEAT     441    452       BNR 3.
FT   REPEAT     521    532       BNR 4.
FT   REPEAT     562    573       BNR 5.
FT   DOMAIN     803    977       5 X APPROXIMATE YWTD REPEATS.
FT   REPEAT     803    806       1.
FT   REPEAT     847    850       2.
FT   REPEAT     891    894       3.
FT   REPEAT     934    937       4.
FT   REPEAT     974    977       5.
FT   DOMAIN    1026   1072       EGF-LIKE.
FT   DOMAIN    1076   1114       LDL-RECEPTOR CLASS A 1.
FT   DOMAIN    1115   1155       LDL-RECEPTOR CLASS A 2.
FT   DOMAIN    1156   1194       LDL-RECEPTOR CLASS A 3.
FT   DOMAIN    1197   1237       LDL-RECEPTOR CLASS A 4.
FT   DOMAIN    1237   1273       LDL-RECEPTOR CLASS A 5.
FT   DOMAIN    1273   1317       LDL-RECEPTOR CLASS A 6.
FT   DOMAIN    1323   1361       LDL-RECEPTOR CLASS A 7.
FT   DOMAIN    1366   1405       LDL-RECEPTOR CLASS A 8.
FT   DOMAIN    1417   1455       LDL-RECEPTOR CLASS A 9.
FT   DOMAIN    1469   1508       LDL-RECEPTOR CLASS A 10.
FT   DOMAIN    1512   1551       LDL-RECEPTOR CLASS A 11.
FT   DOMAIN    1556   1645       FIBRONECTIN TYPE-III 1.
FT   DOMAIN    1653   1742       FIBRONECTIN TYPE-III 2.
FT   DOMAIN    1749   1837       FIBRONECTIN TYPE-III 3.
FT   DOMAIN    1842   1927       FIBRONECTIN TYPE-III 4.
FT   DOMAIN    1933   2024       FIBRONECTIN TYPE-III 5.
FT   DOMAIN    2025   2115       FIBRONECTIN TYPE-III 6.
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 29, 2004, 08:45:43 ; Search time 35 Seconds
(without alignments)
678.310 Million cell updates/sec

Title: US-09-982-405-2
Perfect score: 469
Sequence: 1 MIHLGHILFLLLLPVAAAQT.....RPRRSPAQDGKVYINMPGRG 92

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	469	100.0	92	4	Q9UBS1	Q9ubs1 homo sapien
2	458.5	97.8	93	4	Q9UBK5	Q9ubk5 homo sapien
3	458.5	97.8	131	4	Q9Y3Y0	Q9y3y0 homo sapien
4	353.5	75.4	79	6	Q8WNQ9	Q8wnq9 macaca mula
5	285.5	60.9	79	11	Q9QUJ0	Q9quj0 mus musculu
6	283.5	60.4	79	6	Q9GJR5	Q9gjr5 sus scrofa
7	256.5	54.7	71	11	Q9R1E7	Q9r1e7 mus musculu
8	79	16.8	178	13	Q9DED2	Q9ded2 paralichthy
9	79	16.8	182	13	Q9DED1	Q9ded1 paralichthy
10	79	16.8	182	13	Q90ZH4	Q90zh4 paralichthy
11	79	16.8	404	16	Q8G4F6	Q8g4f6 bifidobacte
12	77.5	16.5	597	17	O30225	O30225 archaeoglob
13	77	16.4	278	16	Q9RRQ1	Q9rrq1 deinococcus
14	77	16.4	492	2	Q93HH8	Q93hh8 streptomyce
15	76.5	16.3	1235	11	Q9JLS3	Q9jls3 rattus norv
16	74.5	15.9	156	16	Q9RKZ5	Q9rkz5 streptomyce
17	74	15.8	618	16	Q8P764	Q8p764 xanthomonas
18	73.5	15.7	112	4	Q9UMT3	Q9umt3 homo sapien
19	73.5	15.7	117	16	Q8P869	Q8p869 xanthomonas
20	72.5	15.5	168	13	Q90XD6	Q90xd6 pleurodeles
21	72.5	15.5	378	2	Q8KUG7	Q8kug7 actinosynne
22	72.5	15.5	1062	4	Q9NSW2	Q9nsw2 homo sapien
23	72.5	15.5	1235	4	Q9UL54	Q9ul54 homo sapien
24	72	15.4	591	4	Q96IA0	Q96ia0 homo sapien
25	71.5	15.2	108	6	Q9TU45	Q9tu45 sus scrofa
26	71.5	15.2	210	10	Q8RZ65	Q8rz65 oryza sativ
27	71.5	15.2	382	10	Q93ZK0	Q93zk0 arabidopsis
28	71.5	15.2	640	10	Q9C9Y8	Q9c9y8 arabidopsis
29	71	15.1	396	16	O34597	O34597 bacillus su
30	71	15.1	461	16	Q8P351	Q8p351 xanthomonas
31	71	15.1	699	16	Q9KYU9	Q9kyu9 streptomyce
32	71	15.1	901	16	Q98I04	Q98i04 rhizobium l
33	70.5	15.0	190	16	Q9HUR9	Q9hur9 pseudomonas
34	70	14.9	140	10	Q8H6T0	Q8h6t0 chlamydomon
35	70	14.9	450	16	Q92YS3	Q92ys3 rhizobium m
36	69.5	14.8	113	6	Q8WNQ8	Q8wnq8 macaca mula
37	69.5	14.8	138	10	Q8LGX2	Q8lgx2 oryza sativ
38	69.5	14.8	261	2	Q93R20	Q93r20 acetobacter
39	69.5	14.8	391	2	Q9X684	Q9x684 pseudomonas
40	69.5	14.8	736	10	Q94HB9	Q94hb9 oryza sativ
41	69	14.7	295	16	Q8P399	Q8p399 xanthomonas
42	69	14.7	488	5	Q8T9B9	Q8t9b9 drosophila
43	68.5	14.6	342	5	O44544	O44544 caenorhabdi
44	68.5	14.6	424	16	Q8XPP3	Q8xpp3 ralstonia s
45	68	14.5	93	17	Q97ZV4	Q97zv4 sulfolobus

ALIGNMENTS

RESULT 1
Q9UBS1
ID Q9UBS1 PRELIMINARY; PRT; 92 AA.
AC Q9UBS1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Membrane protein DAP10.
GN DAP10.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99357865; PubMed=10426994;
RA Wu J., Song Y., Bakker A.B., Bauer S., Spies T., Lanier L.L.,
RA Phillips J.H.;
RT "An Activating Immunoreceptor Complex Formed by NKG2D and DAP10.";
RL Science 285:730-732(1999).
DR EMBL; AF072845; AAD46987.1; -.
DR EMBL; AF072844; AAD46986.1; -.
SQ SEQUENCE 92 AA; 9360 MW; 5D257437153A4FB4 CRC64;

Query Match 100.0%; Score 469; DB 4; Length 92;
Best Local Similarity 100.0%; Pred. No. 8.8e-41;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MIHLGHILFLLLLPVAAAQTTPGERSSLPAFYPGTSGSCSGCGSLSLPLLAGLVAADAVA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MIHLGHILFLLLLPVAAAQTTPGERSSLPAFYPGTSGSCSGCGSLSLPLLAGLVAADAVA 60

Qy         61 SLLIVGAVFLCARPRRSPAQDGKVYINMPGRG 92
              ||||||||||||||||||||||||||||||||
Db         61 SLLIVGAVFLCARPRRSPAQDGKVYINMPGRG 92
```

RESULT 2
Q9UBK5

```
ID   Q9UBK5      PRELIMINARY;      PRT;    93 AA.
AC   Q9UBK5;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Transmembrane adapter protein KAP10 (Membrane protein DAP10).
GN   KAP10 OR DAP10.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99458917; PubMed=10528161;
RA   Chang C., Dietrich J., Harpur A.G., Lindquist J.A., Haude A.,
RA   Loke Y.W., King A., Colonna M., Trowsdale J., Wilson M.J.;
RT   "Cutting edge: KAP10, a novel transmembrane adapter protein
RT   genetically linked to DAP12 but with unique signaling properties.";
RL   J. Immunol. 163:4651-4654(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99357865; PubMed=10426994;
RA   Wu J., Song Y., Bakker A.B., Bauer S., Spies T., Lanier L.L.,
RA   Phillips J.H.;
RT   "An Activating Immunoreceptor Complex Formed by NKG2D and DAP10.";
RL   Science 285:730-732(1999).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Yim D., Jie H.-B., Sotiriadis J., Kim Y.-S., Kim K.-S.,
RA   Rothschild M.F., Lanier L.L., Kim Y.B.;
RT   "Molecular cloning of porcine immunoreceptor DAP10 and NKG2D.";
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF172929; AAD50293.1; -.
DR   EMBL; AF122904; AAD47911.1; -.
DR   EMBL; AF285447; AAG29425.1; -.
KW   Transmembrane.
SQ   SEQUENCE   93 AA;  9489 MW;  97786F24F8A2EE44 CRC64;

  Query Match             97.8%;  Score 458.5;  DB 4;  Length 93;
  Best Local Similarity   98.9%;  Pred. No. 1.1e-39;
  Matches   92;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 MIHLGHILFLLLLPVAAAQTTPGERSSLPAFYPGTSGSCSGCGSLSLPLLAGLVAADAVA 60
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Db          1 MIHLGHILFLLLLPVAAAQTTPGERSSLPAFYPGTSGSCSGCGSLSLPLLAGLVAADAVA 60

Qy         61 SLLIVGAVFLCARPRRSPAQ-DGKVYINMPGRG 92
              |||||||||||||||||||| ||||||||||||
Db         61 SLLIVGAVFLCARPRRSPAQEDGKVYINMPGRG 93


RESULT 3
Q9Y3Y0
ID   Q9Y3Y0      PRELIMINARY;      PRT;   131 AA.
AC   Q9Y3Y0;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Hypothetical protein (Fragment).
GN   DKFZP586C1522.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Uterus;
RA   Koehrer K., Beyer A., Mewes H.W., Gassenhuber J., Wiemann S.;
RL   Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL050163; CAB43303.1; -.
KW   Hypothetical protein.
FT   NON_TER       1       1
SQ   SEQUENCE   131 AA;  13468 MW;  D6E32D31658C619D CRC64;

  Query Match             97.8%;  Score 458.5;  DB 4;  Length 131;
  Best Local Similarity   98.9%;  Pred. No. 1.5e-39;
  Matches   92;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         39 MIHLGHILFLLLLPVAAAQTTPGERSSLPAFYPGTSGSCSGCGSLSLPLLAGLVAADAVA 98

Qy         61 SLLIVGAVFLCARPRRSPAQ-DGKVYINMPGRG 92
              |||||||||||||||||||| ||||||||||||
Db         99 SLLIVGAVFLCARPRRSPAQEDGKVYINMPGRG 131


RESULT 4
Q8WNQ9
ID   Q8WNQ9      PRELIMINARY;      PRT;    79 AA.
AC   Q8WNQ9;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   DAP10.
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   LaBonte M.L., Letvin N.L.;
RT   "Identification of Rhesus Monkey DAP10 and DAP12.";
RL   Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF321610; AAL37223.1; -.
SQ   SEQUENCE   79 AA;  7934 MW;  EACECCD07838B8C9 CRC64;

  Query Match             75.4%;  Score 353.5;  DB 6;  Length 79;
  Best Local Similarity   81.7%;  Pred. No. 5.4e-29;
  Matches   76;  Conservative    0;  Mismatches    2;  Indels   15;  Gaps    2;

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Db          1 MIHPGHILFLLLLPVAAAQTTP--------------GSCSGCGSLSLPLLAGLVAADAVA 46

Qy         61 SLLIVGAVFLCARPRRSPAQ-DGKVYINMPGRG 92
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Db         47 SPLIVGAVFLCARPRRSPAQGDGKVYINMPGRG 79


RESULT 5
Q9QUJ0
ID   Q9QUJ0      PRELIMINARY;      PRT;    79 AA.
AC   Q9QUJ0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Transmembrane adapter protein KAP10 (Hematopoietic cell signal
DE   transducer) (DAP10).
GN   KAP10 OR DAP10 OR HCST.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99458917; PubMed=10528161;
RA   Chang C., Dietrich J., Harpur A.G., Lindquist J.A., Haude A.,
RA   Loke Y.W., King A., Colonna M., Trowsdale J., Wilson M.J.;
RT   "Cutting edge: KAP10, a novel transmembrane adapter protein
RT   genetically linked to DAP12 but with unique signaling properties.";
RL   J. Immunol. 163:4651-4654(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 29, 2004, 08:49:08 ; Search time 34 Seconds
(without alignments)
562.348 Million cell updates/sec

Title: US-09-982-405-2
Perfect score: 469
Sequence: 1 MIHLGHILFLLLLPVAAAQT.....RPRRSPAQDGKVYINMPGRG 92

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 789580 seqs, 207824079 residues

Total number of hits satisfying chosen parameters: 789580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
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18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	469	100.0	92	10	US-09-982-405-2	Sequence 2, Appli
2	469	100.0	92	12	US-10-199-672-446	Sequence 446, App
3	469	100.0	92	12	US-10-187-749-446	Sequence 446, App
4	469	100.0	92	12	US-10-194-457-446	Sequence 446, App
5	469	100.0	92	12	US-10-184-642-446	Sequence 446, App
6	469	100.0	92	12	US-10-196-747-446	Sequence 446, App
7	469	100.0	92	12	US-10-173-689-446	Sequence 446, App
8	469	100.0	92	12	US-10-173-690-446	Sequence 446, App
9	469	100.0	92	12	US-10-173-691-446	Sequence 446, App
10	469	100.0	92	12	US-10-173-692-446	Sequence 446, App
11	469	100.0	92	12	US-10-173-694-446	Sequence 446, App
12	469	100.0	92	12	US-10-173-698-446	Sequence 446, App
13	469	100.0	92	12	US-10-173-699-446	Sequence 446, App
14	469	100.0	92	12	US-10-173-707-446	Sequence 446, App
15	469	100.0	92	12	US-10-174-569-446	Sequence 446, App
16	469	100.0	92	12	US-10-174-583-446	Sequence 446, App
17	469	100.0	92	12	US-10-174-587-446	Sequence 446, App
18	469	100.0	92	12	US-10-174-589-446	Sequence 446, App
19	469	100.0	92	12	US-10-174-591-446	Sequence 446, App
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24	469	100.0	92	12	US-10-175-748-446	Sequence 446, App
25	469	100.0	92	12	US-10-175-751-446	Sequence 446, App
26	469	100.0	92	12	US-10-175-754-446	Sequence 446, App
27	469	100.0	92	12	US-10-176-480-446	Sequence 446, App
28	469	100.0	92	12	US-10-176-489-446	Sequence 446, App
29	469	100.0	92	12	US-10-176-754-446	Sequence 446, App
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33	469	100.0	92	12	US-10-176-922-446	Sequence 446, App
34	469	100.0	92	12	US-10-176-924-446	Sequence 446, App
35	469	100.0	92	12	US-10-176-984-446	Sequence 446, App
36	469	100.0	92	12	US-10-179-508-446	Sequence 446, App
37	469	100.0	92	12	US-10-179-512-446	Sequence 446, App
38	469	100.0	92	12	US-10-179-515-446	Sequence 446, App
39	469	100.0	92	12	US-10-173-702-446	Sequence 446, App
40	469	100.0	92	12	US-10-173-703-446	Sequence 446, App
41	469	100.0	92	12	US-10-173-704-446	Sequence 446, App
42	469	100.0	92	12	US-10-174-574-446	Sequence 446, App
43	469	100.0	92	12	US-10-176-486-446	Sequence 446, App
44	469	100.0	92	12	US-10-176-490-446	Sequence 446, App
45	469	100.0	92	12	US-10-176-752-446	Sequence 446, App

ALIGNMENTS

RESULT 1
US-09-982-405-2
; Sequence 2, Application US/09982405
; Patent No. US20020164764A1
; GENERAL INFORMATION:
; APPLICANT: Paul O. Sheppard
; APPLICANT: Betty A. Haldeman
; APPLICANT: Richard D. Holly
; TITLE OF INVENTION: Transmembrane Polypeptide Expressed by
; TITLE OF INVENTION: Lymphocytes
; FILE REFERENCE: 98-43C1
; CURRENT APPLICATION NUMBER: US/09/982,405
; CURRENT FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 09/631,073
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 09/394,767
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: 60/100,865
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-982-405-2

Query Match 100.0%; Score 469; DB 10; Length 92;
Best Local Similarity 100.0%; Pred. No. 1.4e-43;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MIHLGHILFLLLLPVAAAQTTPGERSSLPAFYPGTSGSCSGCGSLSLPLLAGLVAADAVA 60
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Db          1 MIHLGHILFLLLLPVAAAQTTPGERSSLPAFYPGTSGSCSGCGSLSLPLLAGLVAADAVA 60

Qy         61 SLLIVGAVFLCARPRRSPAQDGKVYINMPGRG 92
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RESULT 2
US-10-199-672-446
; Sequence 446, Application US/10199672
; Publication No. US20030148442A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C1
;  CURRENT APPLICATION NUMBER: US/10/199,672
;  CURRENT FILING DATE:  2002-07-18
;  PRIOR APPLICATION NUMBER: US/10/052,586
;  PRIOR FILING DATE: 2002-01-15
;  PRIOR APPLICATION NUMBER: 60/059263
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/059266
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/063120
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063121
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063486
;  PRIOR FILING DATE: 1997-10-21
;  PRIOR APPLICATION NUMBER: 60/063540
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063541
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063544
;  PRIOR FILING DATE: 1997-10-28
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 446
;   LENGTH: 92
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-199-672-446

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  Best Local Similarity   100.0%;  Pred. No. 1.4e-43;
  Matches   92;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MIHLGHILFLLLLPVAAAQTTPGERSSLPAFYPGTSGSCSGCGSLSLPLLAGLVAADAVA 60
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Db         61 SLLIVGAVFLCARPRRSPAQDGKVYINMPGRG 92


RESULT 3
US-10-187-749-446
; Sequence 446, Application US/10187749
; Publication No. US20030153036A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C1
;  CURRENT APPLICATION NUMBER: US/10/187,749
;  CURRENT FILING DATE:  2002-07-01
;  PRIOR APPLICATION NUMBER: US/10/052,586
;  PRIOR FILING DATE: 2002-01-15
;  PRIOR APPLICATION NUMBER: 60/059263
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/059266
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/063120
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063121
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/063486
;  PRIOR FILING DATE: 1997-10-21
;  PRIOR APPLICATION NUMBER: 60/063540
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063541
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/063544
;  PRIOR FILING DATE: 1997-10-28
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 446
;   LENGTH: 92
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-187-749-446

  Query Match             100.0%;  Score 469;  DB 12;  Length 92;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-43;
  Matches   92;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MIHLGHILFLLLLPVAAAQTTPGERSSLPAFYPGTSGSCSGCGSLSLPLLAGLVAADAVA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MIHLGHILFLLLLPVAAAQTTPGERSSLPAFYPGTSGSCSGCGSLSLPLLAGLVAADAVA 60

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Db         61 SLLIVGAVFLCARPRRSPAQDGKVYINMPGRG 92


RESULT 4
US-10-194-457-446
; Sequence 446, Application US/10194457
; Publication No. US20030153037A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3430R1C296
;  CURRENT APPLICATION NUMBER: US/10/194,457
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GenCore version 5.1.6

OM protein - protein search, using sw model

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(without alignments)
185.362 Million cell updates/sec

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Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	469	100.0	92	4	US-09-127-946-8	Sequence 8, Appli
2	454.5	96.9	93	4	US-09-247-155-114	Sequence 114, App
3	285.5	60.9	79	4	US-09-127-946-10	Sequence 10, Appl
4	75	16.0	2214	1	US-08-727-034-7	Sequence 7, Appli
5	74.5	15.9	553	4	US-09-252-991A-32970	Sequence 32970, A
6	73.5	15.7	113	4	US-09-127-946-2	Sequence 2, Appli
7	72	15.4	548	2	US-08-468-576B-19	Sequence 19, Appl
8	72	15.4	548	2	US-08-468-579B-19	Sequence 19, Appl
9	72	15.4	548	3	US-08-468-577B-19	Sequence 19, Appl
10	72	15.4	979	4	US-08-514-213A-2	Sequence 2, Appli
11	70	14.9	114	4	US-09-127-946-6	Sequence 6, Appli
12	69.5	14.8	408	4	US-09-252-991A-27094	Sequence 27094, A
13	69	14.7	111	4	US-09-227-357-235	Sequence 235, App
14	68.5	14.6	81	2	US-08-812-003-2	Sequence 2, Appli
15	68.5	14.6	675	2	US-08-971-036-2	Sequence 2, Appli
16	68.5	14.6	675	3	US-09-096-570-2	Sequence 2, Appli
17	68.5	14.6	675	4	US-09-265-617B-2	Sequence 2, Appli
18	67	14.3	419	4	US-09-252-991A-23245	Sequence 23245, A
19	66	14.1	118	4	US-09-205-258-1060	Sequence 1060, Ap
20	66	14.1	321	4	US-09-252-991A-24270	Sequence 24270, A
21	66	14.1	577	6	5352575-9	Patent No. 5352575
22	65.5	14.0	469	4	US-09-252-991A-30596	Sequence 30596, A
23	65	13.9	147	4	US-09-489-847-137	Sequence 137, App
24	65	13.9	155	4	US-09-489-847-282	Sequence 282, App
25	65	13.9	247	2	US-08-463-911-2	Sequence 2, Appli
26	65	13.9	247	3	US-09-140-804-8	Sequence 8, Appli
27	65	13.9	247	3	US-09-118-408-3	Sequence 3, Appli
28	65	13.9	247	4	US-09-506-855-3	Sequence 3, Appli
29	65	13.9	247	4	US-09-686-838B-8	Sequence 8, Appli
30	65	13.9	247	4	US-09-911-176B-3	Sequence 3, Appli
31	65	13.9	247	4	US-09-619-740-3	Sequence 3, Appli
32	65	13.9	247	4	US-09-776-976-2	Sequence 2, Appli
33	65	13.9	247	4	US-09-776-976-4	Sequence 4, Appli
34	65	13.9	247	4	US-09-506-852-3	Sequence 3, Appli
35	65	13.9	247	4	US-09-909-547-2	Sequence 2, Appli
36	65	13.9	247	4	US-09-909-547-4	Sequence 4, Appli
37	65	13.9	376	1	US-08-253-155A-33	Sequence 33, Appl
38	65	13.9	521	4	US-09-252-991A-18119	Sequence 18119, A
39	64.5	13.8	223	4	US-09-252-991A-26209	Sequence 26209, A
40	64	13.6	358	4	US-09-252-991A-23102	Sequence 23102, A
41	63.5	13.5	448	4	US-09-342-681C-17	Sequence 17, Appl
42	63.5	13.5	448	4	US-09-342-681C-19	Sequence 19, Appl
43	63	13.4	993	1	US-08-348-143-1	Sequence 1, Appli
44	63	13.4	993	1	US-08-571-785-1	Sequence 1, Appli
45	63	13.4	993	4	US-09-192-435-1	Sequence 1, Appli

ALIGNMENTS

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RESULT 1
US-09-127-946-8
; Sequence 8, Application US/09127946
; Patent No. 6416973
;  GENERAL INFORMATION:
;    APPLICANT:  Bakker, Alexander B.H.
;    APPLICANT:  Phillips, Joseph H.
;    APPLICANT:  Lanier, Lewis L.
;    TITLE OF INVENTION:  Mammalian Cell Membrane Proteins;
;    TITLE OF INVENTION:  Related Reagents
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DNAX Research Institute
;      STREET:  901 California Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/127,946
;      FILING DATE:  31-JUL-1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/089,168
;      FILING DATE:  12-JUN-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/069,692
;      FILING DATE:  16-DEC-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/069,639
;      FILING DATE:  15-DEC-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/063,717
;      FILING DATE:  29-OCT-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/054,430
;      FILING DATE:  01-AUG-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ching, Edwin P.
;      REGISTRATION NUMBER:  34,090
;      REFERENCE/DOCKET NUMBER:  DX0763X
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650)852-9196
;      TELEFAX:  (650)496-1200
;  INFORMATION FOR SEQ ID NO:  8:
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;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  92 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-127-946-8

  Query Match             100.0%;  Score 469;  DB 4;  Length 92;
  Best Local Similarity   100.0%;  Pred. No. 6.6e-45;
  Matches   92;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MIHLGHILFLLLLPVAAAQTTPGERSSLPAFYPGTSGSCSGCGSLSLPLLAGLVAADAVA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MIHLGHILFLLLLPVAAAQTTPGERSSLPAFYPGTSGSCSGCGSLSLPLLAGLVAADAVA 60

Qy         61 SLLIVGAVFLCARPRRSPAQDGKVYINMPGRG 92
              ||||||||||||||||||||||||||||||||
Db         61 SLLIVGAVFLCARPRRSPAQDGKVYINMPGRG 92


RESULT 2
US-09-247-155-114
; Sequence 114, Application US/09247155A
; Patent No. 6312922
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, Jean-Baptiste
;  APPLICANT: Duclert, Aymeric
;  APPLICANT: Bougueleret, Lydie
;  TITLE OF INVENTION: Complementary DNAs
;  FILE REFERENCE: GENSET.021A
;  CURRENT APPLICATION NUMBER: US/09/247,155A
;  CURRENT FILING DATE: 1999-02-09
;  EARLIER APPLICATION NUMBER: 60/074,121
;  EARLIER FILING DATE: 1998-02-09
;  EARLIER APPLICATION NUMBER: 60/081,563
;  EARLIER FILING DATE: 1998-04-13
;  EARLIER APPLICATION NUMBER: 60/096,116
;  EARLIER FILING DATE: 1998-08-10
;  EARLIER APPLICATION NUMBER: 60/099,273
;  EARLIER FILING DATE: 1998-10-04
;  NUMBER OF SEQ ID NOS: 182
;  SOFTWARE: Patent.pm
; SEQ ID NO 114
;   LENGTH: 93
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SIGNAL
;   LOCATION: -18..-1
US-09-247-155-114

  Query Match             96.9%;  Score 454.5;  DB 4;  Length 93;
  Best Local Similarity   97.8%;  Pred. No. 2.7e-43;
  Matches   91;  Conservative    1;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 MIHLGHILFLLLLPVAAAQTTPGERSSLPAFYPGTSGSCSGCGSLSLPLLAGLVAADAVA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MIHLGHILFLLLLPVAAAQTTPGERSSLPAFYPGTSGSCSGCGSLSLPLLAGLVAADAVA 60

Qy         61 SLLIVGAVFLCARPRRSPAQD-GKVYINMPGRG 92
              |||||||||||||||||||: ||||||||||
Db         61 SLLIVGAVFLCARPRRSPAQEYGKVYINMPGRG 93


RESULT 3
US-09-127-946-10
; Sequence 10, Application US/09127946
; Patent No. 6416973
;  GENERAL INFORMATION:
;    APPLICANT:  Bakker, Alexander B.H.
;    APPLICANT:  Phillips, Joseph H.
;    APPLICANT:  Lanier, Lewis L.
;    TITLE OF INVENTION:  Mammalian Cell Membrane Proteins;
;    TITLE OF INVENTION:  Related Reagents
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DNAX Research Institute
;      STREET:  901 California Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/127,946
;      FILING DATE:  31-JUL-1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/089,168
;      FILING DATE:  12-JUN-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/069,692
;      FILING DATE:  16-DEC-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/069,639
;      FILING DATE:  15-DEC-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/063,717
;      FILING DATE:  29-OCT-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/054,430
;      FILING DATE:  01-AUG-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ching, Edwin P.
;      REGISTRATION NUMBER:  34,090
;      REFERENCE/DOCKET NUMBER:  DX0763X
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650)852-9196
;      TELEFAX:  (650)496-1200
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  79 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-127-946-10

  Query Match             60.9%;  Score 285.5;  DB 4;  Length 79;
  Best Local Similarity   67.4%;  Pred. No. 1.2e-24;
  Matches   60;  Conservative    8;  Mismatches    6;  Indels   15;  Gaps    2;

Qy          5 GHILFLLLLPVAAAQTTPGERSSLPAFYPGTSGSCSGCGSLSLPLLAGLVAADAVASLLI 64
              |::|||||||||:||             ::|||||:|||||||||||||| ||||
Db          5 GYLLFLLLLPVAASQT-------------SAGSCSGCGTLSLPLLAGLVAADAVMSLLI 50

Qy         65 VGAVFLCARPRRSPAQ-DGKVYINMPGRG 92
              || ||:| ||   ||| ||:||||||||
Db         51 VGVVFVCMRPHGRPAQEDGRVYINMPGRG 79


RESULT 4
US-08-727-034-7
; Sequence 7, Application US/08727034
; Patent No. 5665872
;  GENERAL INFORMATION:
;    APPLICANT:  SAITO, YASHUSHI
;    APPLICANT:  IWASAKI, AKIO
;    APPLICANT:  ARAI, KOICHI
;    APPLICANT:  YAMAZAKI, HIROYUKI
;    TITLE OF INVENTION:  NOVEL LDL RECEPTOR ANALOG PROTEIN AND
;    TITLE OF INVENTION:  THE GENE CODING THEREFOR
;    NUMBER OF SEQUENCES:  8
```

```
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/727,034
;      FILING DATE:  08-OCT-1996
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 261440/1995
;      FILING DATE:  09-OCT-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 102451/1996
;      FILING DATE:  24-APR-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  OBLON, NORMAN F.
;      REGISTRATION NUMBER:  24,618
;      REFERENCE/DOCKET NUMBER:  80-079-0
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-413-3000
;      TELEFAX:  703-413-2220
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;     LENGTH: 2214 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-727-034-7

  Query Match             16.0%;  Score 75;  DB 1;  Length 2214;
  Best Local Similarity   26.3%;  Pred. No. 16;
  Matches   26;  Conservative   10;  Mismatches   31;  Indels   32;  Gaps    4;

Qy         20 TTPGERSSLPAFYPGTSGSC-------------SGCGSLSLPLLAGLVAADAVASLLIV 65
              :|||  : || :|  :||:|               |   : |||| : ||     |
Db       1412 STPGPSTCLPNYYRCSSGTCVMDTWVCDGYRDCADGSDEEACPLLANVTAASTPTQL--- 1468

Qy         66 GAV----FLCARPR----------RSPAQDGKVYINMP 89
              |     | | :|:               |||:   | |
Db       1469 GRCDRFEFECHQPKTCIPNWKRCDGHQDCQDGRDEANCP 1507


RESULT 5
US-09-252-991A-32970
; Sequence 32970, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 32970
;   LENGTH: 553
;   TYPE: PRT
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32970

  Query Match             15.9%;  Score 74.5;  DB 4;  Length 553;
  Best Local Similarity   26.4%;  Pred. No. 3.2;
  Matches   29;  Conservative   12;  Mismatches   30;  Indels   39;  Gaps    4;

Qy          9 FLLLLPVAAAQTTPGERSS----------------------LPAFYPGTSGSCSGCGSL 45
              |||| |   |:|   || :                      |  :|   |  :|   :
Db        388 FLLLAPDRRARTDHAERPAAGNAQCRKGFGGEELADRRAQHGAPVAHPRV-GGLAGALEV 446

Qy         46 SLPLLAGLV------AADAVASLLIVGAVFLCA---------RPRRSPAQ 80
               :|:|||||       | |||   ::||  :           ||:  ||:
Db        447 QVPVLAGLVDHLAEQQAAAVAQARVIGAELVAGIHHRPRLGLRPQLVPAE 496


RESULT 6
US-09-127-946-2
; Sequence 2, Application US/09127946
; Patent No. 6416973
;  GENERAL INFORMATION:
;    APPLICANT:  Bakker, Alexander B.H.
;    APPLICANT:  Phillips, Joseph H.
;    APPLICANT:  Lanier, Lewis L.
;    TITLE OF INVENTION:  Mammalian Cell Membrane Proteins;
;    TITLE OF INVENTION:  Related Reagents
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DNAX Research Institute
;      STREET:  901 California Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/127,946
;      FILING DATE:  31-JUL-1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/089,168
;      FILING DATE:  12-JUN-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/069,692
;      FILING DATE:  16-DEC-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/069,639
;      FILING DATE:  15-DEC-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/063,717
;      FILING DATE:  29-OCT-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/054,430
;      FILING DATE:  01-AUG-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ching, Edwin P.
;      REGISTRATION NUMBER:  34,090
;      REFERENCE/DOCKET NUMBER:  DX0763X
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650)852-9196
;      TELEFAX:  (650)496-1200
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  113 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-127-946-2

  Query Match             15.7%;  Score 73.5;  DB 4;  Length 113;
  Best Local Similarity   36.8%;  Pred. No. 0.6;
  Matches   25;  Conservative    8;  Mismatches   26;  Indels    9;  Gaps    3;
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Qy          10 LLLLPVAAAQTTPGERSSLPAFYPGTSGSCSGCGSLSLPLLAGLVAADAVASLLIVGAVF 69
               |||||:  |       | |           || | ::|  :|||:|  | | ::||  ||:
Db          10 LLLLPLLLAV------SGLRPVQAQAQSDCS-CSTVSPGVLAGIVMGDLVLTVLIALAVY 62

Qy          70 LCAR--PR 75
                 |  ||
Db          63 FLGRLVPR 70
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RESULT 7
US-08-468-576B-19
; Sequence 19, Application US/08468576B
; Patent No. 5955345
; GENERAL INFORMATION:
; APPLICANT: Rabin, Daniel
; TITLE OF INVENTION: PANCREATIC ISLET CELL ANTIGENS
; TITLE OF INVENTION: OBTAINED BY MOLECULAR CLONING
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sprung Kramer Schaefer & Briscoe
; STREET: 660 White Plains Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-5144
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: System 7.5
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,576B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/239,276
; FILING DATE: 05-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,646
; FILING DATE: 08-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/715,181
; FILING DATE: 14-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/441,703
; FILING DATE: 04-DEC-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/312,543
; FILING DATE: 17-FEB-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurt G. Briscoe
; REGISTRATION NUMBER: 33,141
; REFERENCE/DOCKET NUMBER: MDI 251.7-KGB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 332-1700
; TELEFAX: (914) 332-1844
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 548 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-468-576B-19

Query Match 15.4%; Score 72; DB 2; Length 548;
Best Local Similarity 41.8%; Pred. No. 6.1;
Matches 23; Conservative 4; Mismatches 24; Indels 4; Gaps 1;

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Qy          19 QTTPGERSSLPAFYPGTSGSCSGCGSLSLPLLAGLVAADAVASLLIVGAVFLCAR 73
               ||  |:|    |  | |: | |   |    :|  |||   || ||:  || ||| |
Db         163 QTGVGQREEAAAVLPQTAHSTSPMRS----VLLTLVALAGVAGLLVALAVALCVR 213
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RESULT 8
US-08-468-579B-19
; Sequence 19, Application US/08468579B
; Patent No. 5981700
; GENERAL INFORMATION:
; APPLICANT: Rabin, Daniel
; TITLE OF INVENTION: PANCREATIC ISLET CELL ANTIGENS
; TITLE OF INVENTION: OBTAINED BY MOLECULAR CLONING
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sprung Kramer Schaefer & Briscoe
; STREET: 660 White Plains Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-5144
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: System 7.5
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,579B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/239,276
; FILING DATE: 05-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,646
; FILING DATE: 08-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/715,181
; FILING DATE: 14-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/441,703
; FILING DATE: 04-DEC-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/312,543
; FILING DATE: 17-FEB-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurt G. Briscoe
; REGISTRATION NUMBER: 33,141
; REFERENCE/DOCKET NUMBER: MDI 251.5-KGB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 332-1700
; TELEFAX: (914) 332-1844
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 548 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-468-579B-19

Query Match 15.4%; Score 72; DB 2; Length 548;
Best Local Similarity 41.8%; Pred. No. 6.1;
Matches 23; Conservative 4; Mismatches 24; Indels 4; Gaps 1;

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Qy          19 QTTPGERSSLPAFYPGTSGSCSGCGSLSLPLLAGLVAADAVASLLIVGAVFLCAR 73
               ||  |:|    |  | |: | |   |    :|  |||   || ||:  || ||| |
Db         163 QTGVGQREEAAAVLPQTAHSTSPMRS----VLLTLVALAGVAGLLVALAVALCVR 213
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RESULT 9
US-08-468-577B-19
; Sequence 19, Application US/08468577B
; Patent No. 6001804
; GENERAL INFORMATION:
; APPLICANT: Rabin, Daniel
; TITLE OF INVENTION: PANCREATIC ISLET CELL ANTIGENS
; TITLE OF INVENTION: OBTAINED BY MOLECULAR CLONING
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sprung Kramer Schaefer & Briscoe
; STREET: 660 White Plains Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-5144
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: System 7.5
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,577B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/239,276
; FILING DATE: 05-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,646
; FILING DATE: 08-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/715,181
; FILING DATE: 14-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/441,703
; FILING DATE: 04-DEC-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/312,543
; FILING DATE: 17-FEB-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurt G. Briscoe
; REGISTRATION NUMBER: 33,141
; REFERENCE/DOCKET NUMBER: MDI 251.8-KGB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 332-1700
; TELEFAX: (914) 332-1844
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 548 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-468-577B-19

Query Match 15.4%; Score 72; DB 3; Length 548;
Best Local Similarity 41.8%; Pred. No. 6.1;
Matches 23; Conservative 4; Mismatches 24; Indels 4; Gaps 1;

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Qy         19 QTTPGERSSLPAFYPGTSGSCSGCGSLSLPLLAGLVAADAVASLLIVGAVFLCAR 73
              ||  |:|    |  | |: | |   |    :|  |||   || ||:  || || |
Db        163 QTGVGQREEAAAVLPQTAHSTSPMRS----VLLTLVALAGVAGLLVALAVALCVR 213
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RESULT 10
US-08-514-213A-2
; Sequence 2, Application US/08514213A
; Patent No. 6391651
; GENERAL INFORMATION:
; APPLICANT: Maclaren, No. 63916511
; APPLICANT: No. 6391651kins, Abner
; APPLICANT: Lan, Michael
; TITLE OF INVENTION: MATERIALS AND METHODS FOR DETECTION AND
; TITLE OF INVENTION: TREATMENT OF INSULIN-DEPENDENT DIABETES
; FILE REFERENCE: 14014.0199
; CURRENT APPLICATION NUMBER: US/08/514,213A
; CURRENT FILING DATE: 1995-08-11
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 979
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Aritficial Sequence: /No. 6391651e =
; OTHER INFORMATION: synthetic construct
US-08-514-213A-2

Query Match 15.4%; Score 72; DB 4; Length 979;
Best Local Similarity 41.8%; Pred. No. 12;
Matches 23; Conservative 4; Mismatches 24; Indels 4; Gaps 1;

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Qy         19 QTTPGERSSLPAFYPGTSGSCSGCGSLSLPLLAGLVAADAVASLLIVGAVFLCAR 73
              ||  |:|    |  | |: | |   |    :|  |||   || ||:  || || |
Db        551 QTGVGQREEAAAVLPQTAHSTSPMRS----VLLTLVALAGVAGLLVALAVALCVR 601
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RESULT 11
US-09-127-946-6
; Sequence 6, Application US/09127946
; Patent No. 6416973
; GENERAL INFORMATION:
; APPLICANT: Bakker, Alexander B.H.
; APPLICANT: Phillips, Joseph H.
; APPLICANT: Lanier, Lewis L.
; TITLE OF INVENTION: Mammalian Cell Membrane Proteins;
; TITLE OF INVENTION: Related Reagents
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/127,946
; FILING DATE: 31-JUL-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/089,168
; FILING DATE: 12-JUN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/069,692
; FILING DATE: 16-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/069,639
; FILING DATE: 15-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/063,717
; FILING DATE: 29-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/054,430
; FILING DATE: 01-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0763X
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1200
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-127-946-6

Query Match 14.9%; Score 70; DB 4; Length 114;
Best Local Similarity 33.8%; Pred. No. 1.5;
Matches 23; Conservative 9; Mismatches 26; Indels 10; Gaps 3;

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Qy          7 ILFL-LLLPVAAAQTTPGERSSLPAFYPGTSGSCSGCGSLSLPLLAGLVAADAVASLLIV 65
              :||| :|| |       :  : |         |  | |:|  :|||:|  | | :|||
Db         10 LLFLPVLLTVGGLSPVQAQSDTFP--------RCD-CSSVSPGVLAGIVLGDLVLTLLIA 60

Qy         66 GAVFLCAR 73
                ||:  |
Db         61 LAVYSLGR 68


RESULT 12
US-09-252-991A-27094
; Sequence 27094, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 27094
;   LENGTH: 408
;   TYPE: PRT
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27094

  Query Match             14.8%;  Score 69.5;  DB 4;  Length 408;
  Best Local Similarity   33.8%;  Pred. No. 8;
  Matches   25;  Conservative   10;  Mismatches   32;  Indels    7;  Gaps    3;

Qy          4 LGHILFLLLLPVAAAQTTPGERSSLPAFYPGTS--GSCSGCGSLSLPLLAGLVAADAVAS 61
              | |:|  :  : :|||     | :||  : ||   |   |   | || :  :|    ||
Db        259 LDHLLAMFAVGLWAAQQQGAARLALPCTFVGTMLVGGLLGFEGLQLPFMDTGIA----AS 314

Qy         62 LLIVG-AVFLCARP 74
              :| :|  | |  ||
Db        315 VLALGLCVALAVRP 328


RESULT 13
US-09-227-357-235
; Sequence 235, Application US/09227357
; Patent No. 6342581
; GENERAL INFORMATION:
;  APPLICANT: Fischer et al.
;  TITLE OF INVENTION: 123 Human Secreted Proteins
;  FILE REFERENCE: PZ010P1
;  CURRENT APPLICATION NUMBER: US/09/227,357
;  CURRENT FILING DATE: 1999-01-08
;  EARLIER APPLICATION NUMBER: PCT/US98/13684
;  EARLIER FILING DATE: 1998-07-07
;  EARLIER APPLICATION NUMBER: 60/051,926
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/052,793
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/051,925
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/051,929
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/052,803
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/052,732
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/051,931
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/051,932
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/051,916
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/051,930
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/051,918
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/051,920
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/052,733
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/052,795
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/051,919
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/051,928
;  EARLIER FILING DATE: 1997-07-08
;  EARLIER APPLICATION NUMBER: 60/055,722
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/055,723
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/055,948
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/055,949
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/055,953
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/055,950
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/055,947
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/055,964
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/056,360
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/055,684
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/055,984
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/055,954
;  EARLIER FILING DATE: 1997-08-18
;  EARLIER APPLICATION NUMBER: 60/058,785
;  EARLIER FILING DATE: 1997-09-12
;  EARLIER APPLICATION NUMBER: 60/058,664
;  EARLIER FILING DATE: 1997-09-12
;  EARLIER APPLICATION NUMBER: 60/058,660
;  EARLIER FILING DATE: 1997-09-12
;  EARLIER APPLICATION NUMBER: 60/058,661
;  EARLIER FILING DATE: 1997-09-12
;  NUMBER OF SEQ ID NOS: 672
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 235
;   LENGTH: 111
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-227-357-235

  Query Match             14.7%;  Score 69;  DB 4;  Length 111;
  Best Local Similarity   35.3%;  Pred. No. 1.8;
  Matches   24;  Conservative    8;  Mismatches   26;  Indels   10;  Gaps    3;

Qy         10 LLLLPVAAAQTTPGERSSLPAFYPGTSGSCSGCGSLSLPLLAGLVAADAVASLLIVGAVF 69
              |||||:  |          |           || |::|  :|||:|  | | ::||  ||:
Db         10 LLLLPLLLA-------VGLRPVQAQAQSDCS-CSTVSPGVLAGIVMGDLVLTVLIALAVY 61

Qy         70 LCAR--PR 75
                |  ||
Db         62 FLGRLVPR 69


RESULT 14
US-08-812-003-2
; Sequence 2, Application US/08812003
; Patent No. 5952197
```

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;  GENERAL INFORMATION:
;    APPLICANT:  Ni, Jian
;    TITLE OF INVENTION:  Chemotactic Cytokine III
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  HUMAN GENOME SCIENCES, INC.
;      STREET:  9410 KEY WEST AVENUE
;      CITY:  ROCKVILLE
;      STATE:  MARYLAND
;      COUNTRY:  USA
;      ZIP:  20850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/812,003
;      FILING DATE:  05-MAR-1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROOKES, A. ANDERS
;      REGISTRATION NUMBER:  36,373
;      REFERENCE/DOCKET NUMBER:  PF256
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  301-309-8504
;      TELEFAX:  301-309-8512
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  81 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-812-003-2

  Query Match             14.6%;  Score 68.5;  DB 2;  Length 81;
  Best Local Similarity   44.7%;  Pred. No. 1.4;
  Matches   17;  Conservative    3;  Mismatches   13;  Indels    5;  Gaps    1;

Qy          5 GHILFLLLLPVAAAQTTPGERSSLPAFYPGTSGSCSGC 42
              |  | |||:||||||  ||   |       |: :|  |
Db         19 GAALLLLLIPVAAAQEPPGAACS-----QNTNKTCEEC 51


RESULT 15
US-08-971-036-2
; Sequence 2, Application US/08971036
; Patent No. 5866684
;  GENERAL INFORMATION:
;    APPLICANT:  Attwood, Michael R
;    APPLICANT:  Hurst, David N
;    APPLICANT:  Jones, Philip S
;    APPLICANT:  Kay, Paul B
;    APPLICANT:  Raynham, Tony M
;    APPLICANT:  Wilson, Francis X
;    TITLE OF INVENTION:  Amino Acid Derivatives
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  N.J.
;      COUNTRY:  U.S.A.
;      ZIP:  07110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/971,036
;      FILING DATE:  14-NOV-1997
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9623908.2
;      FILING DATE:  18-NOV-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kreisler, Lewis J
;      REGISTRATION NUMBER:  38522
;      REFERENCE/DOCKET NUMBER:  RAN 4430/073
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (973) 235-4387
;      TELEFAX:  (973) 235-2363
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  675 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
US-08-971-036-2

  Query Match             14.6%;  Score 68.5;  DB 2;  Length 675;
  Best Local Similarity   30.5%;  Pred. No. 19;
  Matches   25;  Conservative   14;  Mismatches   30;  Indels   13;  Gaps    3;

Qy         13 LPVAAAQTTP-----GERSSLPAFYPGTSGSCSGCGSLSLP---LLAGLVAADA-----V 59
              :|| : :||        : || ||   |  |   | | |:    |: |::|| |
Db        582 VPVESMETTMRSPVFTDNSSPPAVCMGGGGGGGGGGGGSMSTWVLVGGVLAALAAYCLTT 641

Qy         60 ASLLIVGAVFLCARPRRSPAQD 81
               |::||| : |  :|   | ::
Db        642 GSVVIVGRIVLSGKPAIIPDRE 663


Search completed: January 29, 2004, 08:50:12
Job time : 22 secs
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